STIC-Biotech/ChemLib

97526

From: Sent:

Rao, Manjunath N.

Thursday, June 26, 2003 11:20 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 09/762,767

Fr m: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 6-26-03

Please search the following as soon as possible for application with serial number 09/762,767

- 1. SEQ ID NO:1 and 3, against all <u>commercial nucleic acid databases</u> including <u>issued patents database</u> and <u>pending application database</u> and provide a <u>print of all results</u>.
- 2. SEQ ID NO: 2 and 4, against all <u>commercial protein databases</u> including <u>issued patents database</u> and <u>pending application database</u> and provide a <u>print of all results</u>.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

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Result
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Maximum Match 100%
Listing first 45 summaries
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Human adenylate	46	23	1103		310.5
Human adenylyl	AAE17129	23	1086		312
_	AAB02006	21	1090		319
Rat adenylyl cycla	AAR94560	17	1090	8.9	319
Type VII a	AAB02011	21	1099		319.5
н	AAB02008 ·	21	1064		322
	AAE14742	23	1086		322.5
	AAE02938	22	1086		322.5
Human adenylate	AAE14741	23	887		322.5
Human adenylate	AAU01924	22	1077		325.5
Partial am:	AAG67400	22	273		356
Drosophila melanog	ABB69902	22	649		396
ద	ABB69903	22	669		397
Amino acid	AAB83941	22	949		398.5
Amino acid	AAB83939	22	1151	11.2	403.5
GC-C. Rattus ratt	AAR38861	14	1075	11.3	407.5
_	AAU08788	23	1073	11.4	408.5
TS	AAW37371	19	1073	11.4	408.5
	AAW32063	18	1073	11.4	408.5
	ABG03067	22	887	11.4	408.5
	ABB61743	22	566	11.7	421.5
	ABB71674	22	1525	11.8	423.5
	ABB64661	22	975	12.4	445
Drosophila melanog	ABB71206	22	1076	12.6	453
phila	ABB72034	22	1172	12.7	456.5
	ABB11783	22	1075	12.7	456.5
	AAU11281	23	1061	12.7	456.5
נם	AAU11280	23	1061	12.7	456.5
GC-A. Rattus	AAR38862	14	1029	12.7	457.5
Þ	AAR10867	12	1047	12.8	460
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	Modified-site		Modified-site		Modified-site		Modified-site		Modified-site	Key	Homo sapiens.		neurological; vision; reproductive; smooth muscle.	cell proliferat	hypotensive; ge	<pre>anti-infertility; anti-allergic; vasotropic; immunosuppressive</pre>	anti-Alzheimer'	anti-sclerotic;	immunomodulator	anti-arterioscl	Cyclic nucleoti	ı	Human cyclic nucleotide-associated protein-3 (CNAP-3).	04-JUL-2000 (f		AAY70475;	4/5 AAY70475 standard; Protein; 690 AA.	I P
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Human soluble guan Drosophila melanog Drosophila melanog Drosophila melanog

Amino

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Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders -
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ty with human soluble guanylate cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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QQGTNSKPCFQKKDVEDGNANFLGKASGID
                                                                      VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
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                                                                                              08-DEC-2000;
24-JAN-2001;
16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
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08-DEC-2000;
                                                                                     04-MAY-2001;
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2002-471335/50.
)В; ABK92259.
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                                   Mack
                                                          BIOTECHNOLOGY INC
                                                                                  2000US-0733742.

2001US-26957P.

2001US-276791P.

2001US-276888P.

2001US-281922P.

2001US-281922P.

2001US-2862146.

2001US-288589P.
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                                  DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a bhological sample from the patient with comprises contacting a bhological sample from the patient with comprises contacting a bhological sample from the patient with comprises contacting a bhological sample from the patient with contact them. The prostate cancer-associated polynucleotide sequences to them. The prostate cancer-associated polynucleotide sequences contact the prostate cancer and are derived from the tissues of various corganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating constate cancer in mammals. The prostate cancer associated genes are cuseful for diagnosing or treating prostate cancer, as well as for constate cancer. The nucleic acid sequences are particularly useful congene therapy, as a vaccine or in antisense applications.
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Best Local Similarity
Matches 690; Conserv
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QQGTNSKPCFQKKDVEDGNANFLGKASGID
                                                                                                                                                                                         TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHK
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                                                              VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
                                                                                                                                   ESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNN
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                                            VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
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Pred. No. 0;
0; Mismatches
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MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESLP

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                                                                                                                                                  The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in corganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer, as reparticularly useful in gene therapy, as a vaccine or in antisense applications.

C ABG61800-ABG61944 represent prostate cancer-associated proteins.
Query Match
Best Local S
Matches 625
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08-DEC-2000;
08-DEC-2000;
24-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a prostate cancer-associated transcript in a cell in patient, useful for diagnosing prostate cancer (PC) or screenin modulators of PC, by determining if prostate cancer-associated are expressed in a prostate tissue
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30-APR-2001;
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16-MAR-2001;
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DB; ABK92193.
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2000US-0733728.

2000US-0733728.

2000US-263957P.

2001US-276889.

2001US-276889.

2001US-281922P.

2001US-281922P.

2001US-286214P.

2001US-288589P.
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                              88.3%;
90.7%;
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Score 3171.5; DB Pred. No. 1.1e-294 0; Mismatches 37
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23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                               developmental
                                      2000US-191637P.
2000US-0614150.
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                               biology; cell signalling;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic a
genes from Drosophila
interactions -
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mes 247; Conserv
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                                                                                                                                                                                                                     GSLKALTRMLYKVDVNIKIEP--VEGDARRY---RYLFSLVKDNSQTMLMGRPTSVSKTI 244
                                                                          ALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV 612
                                                                                                                                                                  KATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTA
                                                                                                                                                                                                                                                                                                    EE-----YFEILTPK-INQTFSGIMTMLNMQFVVRVRRWDNSVKKSSRVMDLKGQMIY 372
                                                                                                                                                                                                                                                                                                                                                                                                          GIIKAAAHVLYETEVEVSLMPPCFHNDCSEFVNQPYLLYSVH-----MKSTKP-SLSPSK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                    QEFIGSIDGVYDVLK----LQEED----VTDTGFVCAGEGE----LIFTSERPVIAWLLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSCANYDYLADIQELLLKMDEASASEILV-----LLGEELITCCCTGIIERAFRCLGTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALEDEELSDDALTLTHLQMAIQLLTAPSNEDLNTAVTSLVAKYRQNWPNIHKLKLDPQTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLPORKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAK------HKIK---ESR 106
            ALKINVSPTTKDWLTKHEGFEFELQPRDPSFLPKEFPN--PGGTETCYFLESFR
                                   PRKINVSPTTYRLLKDCPGFVF -- TPRSREELPPNFPSEIPG--- ICHFLDAYQ
                                                                                                               ICSRATPFMVISMLEGLYKDFDEFCDFFDVYKVETIGDAYCVASGLHRASIYDAHKVAWM
                                                                                                                              ICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALM
                                                                                                                                                                                                                                                                           ADFGCQATTYFDFKRPKGLTMKFRDIVRRTYTPFLIGLNNPPGAVDFPAIGLEIKGQMVH
                                                                                                                                                                                                                                                                                                                             PETVQRSNSSNASDLQMNSSSFCKMFPWHFIMNEQLELVQLGRGFSKLY------KPYM
                                                                                                                                                                                                                                                                                                                                                         PQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDFLNSFS----TLLKQSSHCQEAGKRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSLEREDFEKTIAE-----QAVAAGVPVEVIKESLGEEVFKICYEE-DENILGVVGGTL 159
                                                              ALKMIDACSKHITHDGEQIKMRIGLHTGTVLAGVVGRKMPRYCLFGHSVTIANKFESGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %; Score 991.5;
%; Pred. No. 1.7
117; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting for elucidating cell signalling
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The invention
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and cell-cell
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Matches 207
                                                                                                                                                                                                                                                                                                                                This invention describes novel purified human soluble guanylate cyclase alphal/betal (hsCcalphal/betal). The products of the invention have antharteriosclerotic, vasotropic and hypotensive activity. Nucleic acid sequences encoding the alphal and/or betal subunit are useful for somatic gene therapy of arteriosclerosis and restenosis, ischemia (infarct), peripheral arterial occlusive disease and arterial hypertension. Antibodies to hsGcalphal/betal can be used for diagnosis of aberrant hsGCalphal/betal expression in human tissues. This sequence represents the human soluble guanylylcyclase betal subunit described in the method of the human soluble guanylylcyclase betal subunit described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; guanylylcyclase alphal; hsGCalphal; hsGCbetal; soluble; guanylylcyclase betal; antiarteriosclerotic; vasotropic; hypoten gene therapy; arteriosclerosis; restenosis; ischemia; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 16-17;
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human soluble guanylate cyclase alphal/betal and the nucleic acid encoding the subunits, useful for producing diagnostic antibodies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt H,
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                                                                                                                                                                                                                                                                                                                         the invention.
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DB; AAZ88939.
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EEYFEILTPKINGTFSGIMTMLNMQFVVRVRRWDNSVKK---
                                                                                                        LILPGIIKAAAHVLYETEVEVSLM----PPCFHNDCSEFVNQPYLLYSVHMKSTKPS---
                                                                                                                                                           VVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDASILCLDKE-DDFLHVYYFFPKRTTS
                                                                                                                                                                                     QLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEIL-QMFGKMFFVFCQESGYDTILR
                                                                                                                                                                                                                KIKESRKSLEREDFEKTIAEQAVAAGVPV-----EVIKESLGEEVFKICYEED-ENILG
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                        EDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVTQCGNAIYRVLPQLQ-PGNCSL
                                                                               DIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQ------
                                                                                                                                  VLGSNVREFLQNLDAL - - - - - HDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGLQ
                                                   ----LSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNF
                                                                                                                                                                                                                                                                                               619 AA;
                                                                                                                                                                                                                                            Conservative
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11-JUL-2000;
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DB; ABL02252.
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

invention relates to an isolated nucleic acid detection reagent

is

Disclosure; SEQ ID

NO 1239;

21pp + Sequence Listing; English

specification,

The sequence data for this patent did not form

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                        YCLFGNNVTLANKFESCSVPRKINVSPTT-----YRLL-----KDCPGFVFTPR
                                                                                                                      AGGLHKESDTHAVQIALMALKMMELSDEVMSPH-GEPIKMRIGLHSGSVFAGVVGVKMPR 593
                                                                                                                                                                                                                                                                                              RAQDGLKKRLG---KLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQ--VVQA 474
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                    YCLFGDTVNTASRMESTSIAMKVHISESTKVLIGPNYKIIERGEIDVKGKGTMGTYWLEE
                                                                                               VAGAPDKDANHAERVCDMALDMVDAITDLKDPSTGQHLRIRVGVHSGAVVAGIVGLKMPR
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Pred. No. 4e-52;
07; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 5844; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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                                            CGELDVYKVETIGDAYCVAGGL-HKESDTHAVQIALMALKMMELSDEVMSPHGEP---IK
                                                                                   ILPRPVAQQLMAGDLVEPEEFSSVTIYFSDIVGFTELCARSSPMDVVNFLNDLYSTFDRI
                                                                                                    IFPCEVAQQLMQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQ
 MRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGF
                            IGFYDVYKVETIGDAYLVVSGLPEPNGDKHAREIALMALDILRAVSSFNLRH-KPEYKIQ
                                                                                                                                               PTFSTIRSNIRTIMKGFCENLMDDLLNRMEQYANNLESLVEEKTRQLSLEKQRTEELLYQ
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Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                The present sequence represents soybean cyst nematode guanylyl cyclase-2 Chemoreceptor, designated HG-gcy-2. Hg-gc-1 polynucleotides and polypeptides are useful as active agents for controlling plant feeding nematodes. They can be used to screen for compounds that have the ability to disrupt parasitic nematode feeding or chemotaxis.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated polynucleotide encoding nematode guanylyl chemoreceptor, useful for controlling plant feeding nema
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N-PSDB; AAF89878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB83940;
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TLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREEL | : | | | | | ::| |:
                                                                   THAVQIALMALKMMELSDEVMSPH--GEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNV
                                                                                                   SDVVSFTTIASKCSPLQVVNLLNNLYTLLDSIIAEFDVYKVETIGDGYLCVSGLPHRNGH
                                                                                                                        SDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAY-CVAGGLHKESD
                                                                                                                                                             LEVYAGSLEEEVEERTKELVEEKKKTDILLYRMLPKQVADKLKLGQSVEPETFDCVTVFF
                                                                                                                                                                            L----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLF 484
                                                                                                                                                                                                                       SPALLHLIKDCWDESPAERPKMETVT-----
                                                                                                                                                                                                                                                  SSAILFLGSPCVD-----RLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKR
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                                                                                                                                                                                                                                                                                           12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de; guanylyl cyclase-1 chemoreceptor; HG-gcy-1;
chemotaxis; HG-gcy-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       69pp; English.
                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                             Score 461; DB 22;
Pred. No. 2.2e-34;
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                               101;
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ALLQSMNTGRSTNLMDHVFNM

858

642

601 978 543 918

Length 1115; Indels

28;

Gaps

σ

nylyl cyclase nematodes -

B

NTAARLESSSKPMRIHISTTTNHFLVNVLG-GFVTQARGEI 1078

닭

974

ALKIHVSSTTKDALDELGCFQLELRGDVEM 1003

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RESULT 11
AAR38863
ID AAR38
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAR38862-63 represent the guanylyl cyclases, GC-A and GC-B, which binds heat stable enterotoxin. These proteins are enterotoxin receptors which may be used as a therapeutic to control intestinal fluid permeation as well as abnormal conditions caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guanylyl cyclase; GC-C; heat stable; mucosa; polyA+ RNA; PCR; enterotoxin binding domain; antibody; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GC-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New purified enterotoxin receptor protein - prods. for treating abnormal conditions cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5237051-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR38863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by bacterially released enterotoxin. The proteins, or antibodies to the proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-272183/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR38863 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diarrhoea. The proteins may be used to isolate l for antagonists of toxin binding. This sequence represented in the specification.
                               613
                                                                                                                                                                   858
                                                                                                                                                                                                                   500
                                                                                                                                                                                                                                                                798
                                                                                                                                                                                                                                                                                                           440
                                                                                                                                                                                                                                                                                                                                                         738
                                                                                                                                                                                                                                                                                                                                                                                                    411 DVVLIGEQARAQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating abnormal conditions of the contract of the contra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.8%;
Similarity 41.9%;
         PRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                                                                                                                           LQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGL-HKESDTHAVQIALMALKMME 558
                                                                                                                                                                                                                                                           TQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTP
                                                                                                                                                                                                                                                                                                  HQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
                                                                                                                                                                                                                                                                                                                                                  ELVLLMERCWAODPTERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEER
                                                                                                                       LSDEVMS-----
                                                                                                                                                                MQVVTLLNDLYTCFDAIIDNFDVYKVETIGDAYMVVSGLPGRNGQRHAPEIARMALALL-
                                                                          --DAVSSFRIRHRPH-DQLRLRIGVHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 3; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schulz S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0623033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0623033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                  -PHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 460; DB 14,
Pred. No. 2.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1025
                                                                                                                                                                                                                                                                                                                                                                                                    -GLKKRLGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enterotoxin; rat; small intestine;
receptor; bacterial enterotoxin;
ligand; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The binding domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , can be used to eliminate isolate ligands and to screen sequence is given as it is
                               642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to develop
sed by bacterially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                               -----LKATLEQA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                916
                                                                                                                                                                                                                                                                                                       499
                                                                                                                                                                                                                                                                                                                                                    797
                                                                                                                                                                                                                                                              857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
AAR10399
    The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR10399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR10399
                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9100292-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPRB;
                                                                                                                                                                                                                                                                                                                            X,
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Modified-site
                            Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc
                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperaldosteronism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Natriuretic Peptide Receptor B
                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                       1991-036711/05.
DB; AAQ10324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 1047 AA.
Fig 1; 49pp;
                                                                                                                   Goeddel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                          89US-0370673
                                                                                                                                                                                                      90WO-US03586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNP; kidney failure;
ism; glaucoma; guanyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                         161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= cytoplasmic domain
/note= "GC and protien kind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     'label=
                                                                                                                                                                                                                                                                                                                                                                               'label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                            'label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                         'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                       label= N-glycos_site
                                                                                                                   Á
                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l= N-glycos_site
   English.
                                                                                                                    Lowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "binds
                                                                                                                                                                                                                                                                                           N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mature NPBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal sequence
                                                                                                                                                                                                                                                                                                                                                  N-glycos_site
                                                                                                                   Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>د</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSSSXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can also be prepd. An analogue, NPRBDKC, comprising only AAs 1-433 of the mature protein, is also claimed, as well as variant described in AAR10867.
                                                                                                                                                                                                                                                                                                                                                                                             AAR10867 standard; Protein; 1047
 Modified-site
                     Modified-site
                                                                                     Modified-site
                                                                                                                                           Domain
                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                               NPRB; ANP; BNP; CNP; hyperaldosteronism;
                                                                                                                                                                                                                                                                                                                                NPRB(Pro655,
                                                                                                                                                                                                                                                                                                                                                     09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                           Modified-site
                                                                Modified-site
                                                                                                                                                                 Domain
                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVVLIGEQARAQD------GLKKRLGK------LKATLEQA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSDEVMS-----PHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL-HKESDTHAVQIALMALKMME
:||:|:|| || || || ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQAYLEEKRKABALLYQILPHSVABQLKRGETVQABAFDSVTIYFSDIVGFTALSABSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKIHVSSTTKDALDELGCFQLELRGDVEM 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQVVTLLNDLYTCFDAIIDNFDVYKVETIGDAYMVVSGLPGRNGQRHAPEIARMALALL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVLLMERCWAQDPAERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- DAVSSFRIRHRPH-DQLRLRIGVHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                Glu656,
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                         CNP;
/label-
277..279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŗ,
                                                                                                                                         /label= transmembrane domain 479..1047
                                                                                                                                                                /note= "binds
456..456
                                                                                                                                                                                               /label= mature
23..455
                                                                                                                                                                                                                      /label= signal sequence
12
                                            195..
                                                                                                                   /note- "GC and
                                                                                                                               /label-
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                     /label=
                                                                         'label=
                                                                                                                                                                                    /label=
                               'label=
                                                                                               'label = N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%;
                                                                                                                                                                                                                                                                                             ; kidney failure; heart failure; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                                                                                                                               Leu663,
          N-glycos_site
                               N-glycos_site
                                                     N-glycos_site
                                                                         N-glycos_site
                                                                                                                               cytoplasmic domain
                                                                                                                                                                                     extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                             Phe664, Ala682).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 460; DB 12;
Pred. No. 2.5e-34;
                                                                                                                                                                          natriuretic
                                                                                                                    protien
                                                                                                                                                                                                           NPBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                      domain
                                                                                                                      kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      642
                                                                                                                                                                         peptides
                                                                                                                    activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                           A, B
                                                                                                                                                                                                                                                                                                         protein kinase;
                                                                                                                                                                           and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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Editor's note: the AAs replaced in the sequence do not correspond to those of NPRB given in the specification (see p.27, 1.23-27; figs. 1 and 2), but instead to AAs in the sequence provided for NPRB (fig. 2). The origin of the AAs to be substituted is not clear; they may be taken from the sequence of rat NPRB (p.8, 1.18; p.9, 1.33) or rat NPRB (p.27, 1.20). The substitution indicated on p.9, 1.33, i.e. "Phe644" is thought to be an error and should read
                                                                                                                                                                                                                                                                                                                                                     The mutant was produced by modifying the DNA encoding the native sequence. The protein has guanyl cyclase (GC) activity protein kinase activity. The DNA can be inserted into express vectors for the prodn. of the NPRB analogue. The protein can used in treatment of natriuretic peptide disorders, and also tisolate peptides using affinity chromatography. Antibodies wi sefinity for NPRB can also be prepd.
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natriuretic protein receptor B - for diagnosis and kidney failure, heart failure, hyperaldosteronism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang
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ALKIHVSSTTKDALDELGCFQLELRGDVEM
                         PRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                             LSDEVMS-----PHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
                                                                                                        HOVETILINDLYTCFDAIIDNFDYYKVETIGDAYMYVSGLPGRNGQRHAPEIARMALALL-
                                                                                                                                                              TQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTP
                                                                                                                                                                           HQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSP
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                                                   --DAVSSFRIRHRPH-DQLRLRIGVHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGQ
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41.9%;
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                                                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                                      Score 460; DB
Pred. No. 2.5e
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.

    for diagnosis and treatment of
hyperaldosteronism, glaucoma etc

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                         642
                                                                                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                         76;
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RESULT 14 AAR38862

995

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RESULT 15
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ID AAU11
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AC AAU11
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Best Local 9
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mucosa; p
binding d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR38862-63 represent the guanylyl cyclases, GC-A and GC-B, which binds heat stable enterotoxin. These proteins are enterotoxin receptors which may be used as a therapeutic to control intestinal fluid permeation as well as abnormal conditions caused intestinal released enterotoxin. The binding domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GC-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified enterotoxin receptor protein - used to develop prods. for treating abnormal conditions caused by bacterially released enterotoxin, partic. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garbers
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        12-MAR-2002
                                            AAU11280;
                                                                               AAU11280 standard; Protein; 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by bacterially released enterotoxin. The binding domain of the proteins, or antibodies to the proteins, can be used to eliminate diarrhoea. The proteins may be used to isolate ligands and to scr for antagonists of toxin binding.
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polyA+ RNA; PCR; enterotoxin
domain; antibody; diarrhoea;
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                                                                                                                                                                                                                                                                                                                                                           NVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL
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                                                                                                                                                                                                                   LFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREEL 642
                                                                                                                                                                                                                                                            PVRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYC
                                                                                                                                                                                                                                                                                              H-KESDTHAVQIALMALKMMEL--SDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYC
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                                                                                                                                                                                LFGDTVNTASRMESNGEALK THLSSETKAVLEEFDGFELELRGDVEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 457.5; DB 14, Pred. No. 4.2e-34; 0; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                         cc encoding the human natriuretic peptide receptor Ayguanylate cyclase A C (atrionatriuretic peptide receptor Ayguanylate cyclase A C (atrionatriuretic peptide receptor A) or NPRI polypeptide. A method for C haplotyping the NPRI gene in an individual comprises identifying the C nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the NPRI haplotypes given in the specification or whether both copies are defined by a haplotype C pairs can be assigned to specific genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a C trait and a haplotype or haplotype pair of the NPRI gene can be cidentified by comparing the frequency of the haplotype pair in a population exhibiting the trait with the frequency of the haplotype cor haplotype pair in a reference population, where a higher haplotype cor haplotype or haplotype pair. NPRI and its corresponding DNA are used the haplotype or haplotype pair. NPRI and its corresponding DNA are used corresponded to the expression and function of NPRI, for use in screening corresponded to the properties of the pair to treat diseases related to NPRI activity, such as higher thaplotype pair. This sequence are also useful for studying the effect of corresponded to the oblogical activity of NPRI as well as on the binding caffinity of candidate drugs targeting NPRI. This sequence represents the human NPRI no INPRI activity of NPRI as well as on the binding caffinity of candidate drugs targeting NPRI. This sequence represents the
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of an individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of the gene \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bentivegna SC,
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                                                                                                                                                                                                                                                                                                                                                                         Sequence
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)B; AAS16995.
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                                                                                                                                                                                                                                                                                                                                                                                                              lty of candidate drugs targeting NPR1. This sequence represents {\tt NPR1} polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           natriuretic
                                                                                                                                                                                                                                                                                                                Similarity
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LFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREEL
                                                                                                                                    DNLLSRMEQYANNLEELVEERTQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFD
                                                                                                                                                                                                                                       DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS
                                                          PVRNGRLHACEVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYC
                                                                                             H-KESDTHAVQIALMALKMMEL--SDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYC
                                                                                                                                                                            NVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGL
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                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c peptide receptor A; haplotyping; cytostatic;
single nucleotide polymorphism; gene therapy;
hypertension; hypotensive.
                                                                                                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                Score 456.5; DB 2
Pred. No. 5.5e-34;
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994 LFGDTVNTASRMESNGEALKIHLSSETKAVLEEFGGFELELRGDVEM 1040

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Search completed: June 27, 2003, 13:03:00 Job time : 39.3713 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

OM protein protein search, using sw model

June 27, 2003, 13:03:07; Search time 19.5034 Seconds (without alignments) 3401.080 Million cell updates/sec

US-09-762-767A-2 3593

Title: Perfect score:

1 MFCTKLKDLKITGECPFSLL.....QKKDVEDGNANFLGKASGID 690

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum Maximum DB DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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411.5	412.5	414	418	418	420.5	423.5	427	428	428.5	428.5	430	434	435	436	438
11.5	11.5	11.5	11.6	11.6	11.7	11.8	11.9	11.9	11.9	11.9	12.0	12.1	12.1	12.1	12.2
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T34187	T28130	T21223	T27564	T24384	S33525	A56699	OYURCP	T42382	A89130	S45636	I59370	T31667	JH0717	T31666	S55279
_	•	_		hypothetical prote	guanylate cyclase	guanylate cyclase	speract receptor p	guanylate cyclase	protein F52E1.4 [i	natriuretic-peptid	guanylate cyclase	guanylate cyclase	guanylate cyclase	natriuretic peptid	guanylate cyclase

ALIGNMENTS

guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - rat
N;Alternate names: guanylate cyclase, soluble, 77K chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A38297
R;Nakane, M.; Arai, K.; Saheki, S.; Kuno, T.; Buechler, W.; Murad, F.
J. Biol. Chem. 265, 16841-16845, 1990
A;Title: Molecular cloning and expression of cDNAs coding for soluble guanylate cycla
A;Reference number: A38297; MUID:91009100; PMID:1698769
A;Accession: A38297; MUID:91009100; PMID:1698769 A;Cross-references: GB:M57405; GB:M36075; NID:g204277; PIDN:AAA41206.1; PID:g204278 C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology C;Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase F;432-660/Domain: guanylate cyclase catalytic domain homology <GCC> Query Match Best Local Similarity Matches 616; Conserva A; Molecule type: mRNA A; Residues: 1-690 <NAK> Conservative 90.0%; Score 3232; DB 1; 89.1%; Pred. No. 4.6e-217; tive 39; Mismatches 34; Length 690; Indels <u>ب</u> Gaps 2;

480	421 AQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKESNV 480	421	γQ
419	SRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQAR	360	Db
420	~	361	Qy
359	LGNGIRRLVNKRDFQGKPNFEEFFEILTPKINQTFSGIMTMLNMQFVIRVRRWDNLVKKS:	300	Ф
360	0,	301	Qy
299	RSECTEFVNQPYLLYSVHVKSTKPSLSPGKPQSSLVIPTSLECKTFPFHFMLDRDLAILQ	240	B
300	HNDCSEFVNQPYLLYSVHMKSTKPSLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQ 300	241	Qy
239	RGRLEDASILCIDKDQDFLNVYYFFFKRTTALLLPGIIKAAARILYESHVEVSLMPPCF	180	В
240	- 17	181	Qy
179	EAIAAGVPVEVLKDSLGEELFKICYEEDEHILGVVGGTLKDFLNSFSTLLKQSSHCQEAE	120	ф
180	G	121	Qy
119	QRKTSRNRVYLHTLAESIGKLIFPEFERLNLALQRTLAKHKIKENRNSSEKEDLERIIAE	60	탕
120	SLEREDFEKTIAE	61	Qy
59	MFCRKFKDLKITGECPFSLLAPGQVPTEPIEEVAGVSESCQATLPTCQEFAE-NAEGSHP	_	В
60	NIQESLP	_	Qy

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guanylate cyclase (EC 4.6.1.2), soluble, 81K chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S23098
R;Gluili, G; Scholl, U; Bulle, F; Guellaen, G.
FEBS Lett. 304, 83-88, 1992
A;Title: Molecular cloning of the cDNAs coding for the two subunits of soluble A;Reference number: S23097; MUID:92316204; PMID:1352257
A;Accession: S23098
A;Molecule type: mANA
A;Residues: 1-717 <GIU>
A;Cross-references: EMBL:X66534; NID:g31683; PIDN:CAA47145.1; PID:g31684
C;Superfamily: Soluble guanylate cyclase; guanylate cyclase catalytic domain
C;Keywords: heterodimer; phosphorus-oxygen lyase
F;430-658/Domain: guanylate cyclase catalytic domain homology <GCC>
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                                                                                  QAVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHCQE---
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Pred. No. 7.9e-
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OYBO77
guanylate cyclase (EC 4.6.1.2), solubre,
N'Alternate names: guanylate cyclase, solu
C; Species: Bos primigenius taurus (cattle
C; Date: 30-Sep-1991 #sequence_revision 30
C'Accession: $10713; A38767
C'Accession: Harteneck, C.; Humbert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: Sivily, C;
R;Koesling, D.; Harteneck, C;
R;Koesling, D;Koesling, D;Koesling, C;
R;Koesling, D;Koesling, C;
R;Koesling, D;Koesling, C;
R;Koesling, D;Koesling, C;
R;Koesling, 
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F; 434-662/Domain:
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A; Molecule type: protein
A; Residues: 118-133;226-232;286-293;319-330;412-417;557-571;629-637 <K
C; Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
C; Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F;434-662/Domain: guanylate cyclase catalytic domain homology <GCC>
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A;Title: The primary structure of the larger subunit of A;Reference number: S10713; MUID:90306336; PMID:1973124
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A; Molecule type: mRNA
A; Residues: 1-691 < KOE1>
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A;Accession: A38767
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| |:|||||:||||||:|:|||||||||:||
QLGHGIRRLMSRRDVQGKPHFDEYFEILTPKISQTFSGIMTMLNMQFLVRVRRWDNSMKK
                                                                                                                                                                                                                                                                                                                                                                           MFCTKLKDLKITGECPFSLLAPGOVPNESSEEAAGSSESCKATVP-ICQDIPEKNIQESL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQA
                                                                                                                                                                                                                                                                                                                  GKRGRLEDASILCLDKEDDFLHVYYFFFFKRTTSLILPGIIKAAAHVLYETEVEVSLMPPC
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RAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSN
                                                                                                                                                                                                           FHQDCREFVDQPCELYSVHIRSARPHPPPGKPVSSLVIPASLFCKTFPFHFMLDRDMSIL
                                                                                                                                                                                                                                FHNDCSEFVNQPYLLYSVHMKSTKPSLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTIL
                                                                                                                                                                                                                                                                                           PRRKTSRSRVYLHTLAESICKLIFPEFERLNLALQRTLAKHKIKENRKSLEREDFEKIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSLEREDFEKTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHFLDAYQQGTNSKPCFQKKDVEDASQFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 4.6.1.2), soluble, alpha-1 chain guanylate cyclase, soluble, 77K cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: X54014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.5%;
86.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3107.5; DB 1
Pred. No. 2.1e-208;
1; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (cattle)
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259 KKIYRLDVEVEQVANEKLCSD-VSNPGNCSCLTFLIKECENTNIMKNLPQGTSQVP 279 TSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNFEEYFEILTPKIN :	Db 27 GECPLSRICWNGSRSPPGPLEPSPAAAAAAAPAPTPAASAAAAAATAGARRVQR 81 Qy 66 RSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSL	B325 B325 Baylate cyclase, soluble, alpha chain - human Species: Homo saplens (man) Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999 Accession: S18325 BS Lett. 292, 217-222, 1991 Fitle: Molecular cloning and expression of a new alpha-subunit of soluble Reference number: S18325; MUID:92070494; PMID:1683630 Reference number: S18325; MUID:92070494; PMID:1683630 Restous: prelininary Molecule type: mRNA Residues: 1-732 <hard <gcc="" catalytic="" cross-references:="" cyclase="" cyclase;="" domain="" embl:x63282;="" guanylate="" homology="" nid:931670;="" pid:931671="" pidn:caa44921.1;="" soluble="" superfamily:=""> Ouery Match 45.5%; Score 1635; DB 2; Length 732; Best Local Similarity 49.4%; Pred. No. 7.9e-106; Matches 355; Conservative 106; Mismatches 200; Indels 58; Gaps</hard>	Db 421 RAQDGLKKRLGKLKATLEQAHQALEEEKRKTVDLLCSIFPSEVARQLWQGHAVQAKRFGN 480 Qy 480 VTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVKVETIGDAYCVAGGLH 539
Qy 273SSLVIPTSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNFEE 322 Db 246 TVQRSNASDLQMNSSSFCKMFPMHFIMNBQLELVQLGRGFSKLYKPYMAD 298 Qy 323YFELLTPK-INQTFSGIMTMLMMQFVVRVRRWDNSKKSSRVMDLKGQMTYIV 374 :	58 SLPQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAK	cyclase: Drospanding property on: JH08 wa, S.; hem. 60; lsolatic ce numbe ce type: e type: e type: eference ental scental scenarios	

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RESULT 6

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N;Alternate names: guanylate cyclase, soluble, Deta-1 chain - rat

N;Alternate names: guanylate cyclase, soluble, 70K chain

C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A31871

R;Nakane, M.; Saheki, S.; Kuno, T.; Ishii, K.; Murad, F.
Biochem. Biophys. Res. Commun. 157, 1139-1147, 1988
A;Title: Molecular cloning of a cDNA coding for 70 kilodalton subunit of solu
A;Reference number: A31871; MUID:89087429; PMID:2905128
A;Recession: A31871; MUID:89087429; PMID:2905128
A;Recession: A31871
A;Molecule type: mRNA
A;Residues: 1-619 <NAK>
A;Cross-references: GB:M2562; NID:g204273; PIDN:AAA41204.1; PID:g204274
C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain
C;Keywords: CGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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   --VYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHS
                                                                                                                                          NALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQL 466
                                                                                                                                                                                                                                                                            TILQFGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNS : | | | | : : | | | : : | | | : : | | : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVTQCGNAIYRVLPQLQ-PGKCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLD
                                                                                                                                                                                                                                                                                                                                              SEFVNQPYLLYSVHMKSTKPS-----LSPSKPQSSLVIPTSLFCKTPPFHFMFDKDM
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                                                                                                                       DATRDLVLLGEQFREEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANEL
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VEKLECEDELTGAEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLH
                                                                                                                                                                                                                            VKK-----
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                                                                                                                                                                                                          -SSRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 795; DB 1; Pred. No. 1.9e-47;
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C; Genetics:
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A;Molecule type: protein
A;Residues: 1-6;28-32;41-45;96-109;337-343;396-406;562-569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-619 <KOE>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett 239, 29-34, 1988
A;Title: The primary structure of the 70 kDa subunit of A;Reference number: S01653; MUID:89031214; PMID:2903071
A;Accession: S01653
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THAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTL
                                                                     VVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDASILCLDKE-DDFLHVYYFFPKRTTS
                                                  NAFCSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCI
                                                                                                                                                                                                                                                      LSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKSECEDELTGTEISCLRLKGQM
                                                                                                                                                                                                                                                                                                                                                                                         DIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEIL-QMFGKMFFVFCQESGYDTILR
                                                                                                                                                                                                                                                                                                                      EDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVTQCGNAIYRVLPQLQ-PGNCSL
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                                                                                                                                                                                                                                                                                       EEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKSS-----RVMDLKGQM
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kidney.

homology

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guanylate cyclase (EC 4.6.1.2), soluble, 70K chain - hum C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text C;Accession: S23097 R;Giuili, G.; Scholl, U.; Bulle, F.; Guellaen, G. REBS Lett. 304, 83-88, 1992 A;Title: Molecular cloning of the cDNAs coding for the tA;Reference number: S23097; MUID:92316204; PMID:1352257 A;Accession: S23097
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic
C;Keywords: heterodimer; phosphorus-oxygen lyase
F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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A;Cross-references: GDB:141992; OMIM:139397
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96; Mismatches
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Blochemistry 29, 10872-10878, 1990
A;Title: A new form of guanylyl cyclase is preferentially expressed in A; Reference number: A36228; MUID:91105012; PMID:1980215
A; Rocession: A36228
A; Molecule type: mRNA
A; Residues: 1-682 < YUE>
A; Cross-references: GB:M57507; GB:J05308; NID:9204279; PIDN:AAA41207.1
A; Experimental source: kidney
C; Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic C; Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F; 360-584/Domain: guanylate cyclase catalytic domain homology <GCC>
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hypothetical protein T04D3.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *t C;Accession: T24458 R;Kershaw, J.
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Pred. No. 5.9e-46;
                                                        15-Oct-1999 #text_change 04-Mar-2000
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submitted to the EMBL Data Library, A; Reference number: Z19893
A; Accession: T24458
A; Status: preliminary; translated if A; Molecule type: DNA
A; Residues: 1-751 (WIL)
A; Cross-references: EMBL: Z81114; Pl
A; Experimental source: Clone T04D3
C; Genetics:
A; Gene: CESP:T04D3.4
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tive 125; Mismatches 239
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RESULT T23721

hypothetical protein M04G12.3 - CC; Species: Caenorhabditis elegans

Caenorhabditis elegans

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R;Lennard, N.
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A; Introns: 11/3; 36/2;
C; Superfamily: soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:299942; PIDN:CAB17073.1; GSPDB:GN00028; A;Experimental source: clone H13N06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-685 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                              AGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREE---
                                                                                                                                                                                        QLKQGLSVEAREYEEATVMFTDVPTFQQIVPLCTPKDIVHLLNELFTKFDRLIGIQKAYK
                                                                                                                                                                                                                                                       F--QGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWD-----NSVKKSSRVMD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSLEREDFEKTIAEQAV------AAGVPVEVIKESLGE--EVFKICYEED--
GKGEMNTYFLLRSFKRSIWEIIDRRRDENCNSIDGYNELREGYVDDVLNKVTQKNSKTC
                                                                                                                            VETVGDSYMSVGGIPDLVDDHCEVICHLALGMVMEARTVCDPITNTPLHIRAGIHSGPVV
                                                                                                                                                         VETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSDEVMSP-HGEPIKMRIGLHSGSVF
                                                                                                                                                                                                                      QLWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSNEEALGTAVVQHSNNYKIRLTHMDFISTFPYHMVVDQDCKIVQVG----RELYNHIPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSTKPSLSPSKPQSSLVIPTSL----FCKTFPFHFMEDKDMTILQEGNGIRRLMNR--RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRPGLYPIVKGVLREAAKRVFKLDVSMTITGRTQRSVQMATGERIEE-HVIFLVKTLNTD
                                                             AGVVGAKMPRYCLFGDTVNTSSRMESHSPIGRIHCSENAKKCAESTGRFEFEPRGRVQIK
                                                                                                                                                                                                                                                                                    IHNALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKRTTSLILPGIIKAAAHVLYETEVEVSL---MPPCFHNDCSEFVNQPYLLYSVHM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDDLIRSMSPNLKGFLDNLDSLHYFIDHVVYKANLRG----PSFRCEDNPDGTITLHYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ENILGYVGGTLKDFLNSFSTLLKQSSH-CQEAGKRGRLEDASILCLDKEDDFLHVYYFF
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                                                                                                                                                                                                                                                                                                                     SENLYEDNIGALALSQSQHLKLKGQMMLMSSGGHIMYLCSPYVTSIPELLQYGLRLTAMP
                                                                                                                                                                                                                                                                                                                                                                                    LLSVGTP-LMRIFEVTRPQIPLDFDSICNFINAVFVLQVKTTPMEFQRNANKRAAQAIEA
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                               -LPPNFPSEIPGI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70/1; 133/2; 179/1 guanylate cyclase;
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Pred. No. 6.8e-33;
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                               CHFLDAYQQ
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domain homology
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Length 1099; Indels

474/3; 523/3

CESP: TO

146;

Gaps

118

164 19;

162 223

276

216

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hypothetical protein T07D1.1 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-C;Accession: T16822 R;Leimbac, D.
                                                                                                                           RESULT
T16822
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A; Introns: 1/3;
C; Superfamily:
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sion: T23721
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                                                                                                                                                                                                                                                                                                                       ARSYMDPVNKTPFLLRIGLHSGTIIAGVVGTKMPRYCLFGETVTLASQMESLGVAGKIQC
                                                                                                                                                                                                                                                                                                                                                     KNIVKLLNEVFFKLDRIVVLRGVYKVETVSDSYMTVSGIPDYTSEHAENMCHVALGMMWE
                                                                                                                                                                                                                                                                                                                                                                                                                                              LQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMEL :: :|| :: :|| :| :|| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THELEVEROKTDSILKDMLPRKIAKQLLSGEHLEPCEY-EATVMFCDLPAFQQIIPVCQP
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                                                                                                                                                                                                                                                                         SPTTYRLLKDCPGFVFTPRSR
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                                                                                                                                                                                                                            SSWTYSKAMETGRFEFSPRGR
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A; Description: The sequence of C. elegans cosmid T07D1.
A; Reference number: Z18584
A; Accession: T16822
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1099 < CLEI>
A; Cross-references: EMBL:U41531; NID:g1109802; PID:g11098
C; Genetics:
A; Gene: CESP:T07D1.1
A; Introns: 26/3; 94/3; 144/2; 200/3; 239/2; 278/3; 344/1;
                                                                                                                    RESULT 14
T18984

Cypothetical protein C06B3.8 - Caenorhabditis elegans
Cypothetical protein C06B3.8 - Caenorhabditis elegans
Cypothetical protein C06B3.8 - Caenorhabditis elegans
Cypothetical protein C05B3.8 - Caenorhabditis elegans
Cypothetical protein C05B3.8 - Caenorhabditis elegans
Cypothetical protein C05B3.8 - Caenorhabditis elegans
Cypothetical protein C06B3.8 -
submitted to the EMBL Data
A; Reference number: Z19056
A; Accession: T18984
A; Status: preliminary; trar
A; Molecule type: DNA
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A; Residues: 1-699 <WIL>
A; Cross-references: EMB|
A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                         protein C54E4.3 [imported] - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 10-May-2001 #sequence_revision 10-May-2001 #C:Accession: F88642
                                                                                                                          A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology R;Reference number: A75000; MUID:99069613; PMID:981916
A;Note: see websites genome.wustl.edu/gsc/C_elgans/ and www.sanger.ac.uk/Projects/C_elaky.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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R;anonymous, The C. elec
Science 282, 2012-2018,
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C; Superfamily: soluble guany!
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                           Molecule type: DNA
Residues: 1-583 <570>
Cross-references: GB:chr_IV; PIDN:AAB92031.1;
                                                                                         Status: preliminary
                                                                                                            Note: published errata appeared Accession: F88642
Genetics:
                   Note: Similar
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                                                                                                                                                                                                                                                                                                                                                                                                                               ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSR 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAVQIALMALKMMELSDEVMSPHGE-PIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLF 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEVIKESLGEEV---FKICYEED---ENILGVVGGTLKDFLNSFSTLLKQSSH-CQEAGKR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDLPAFQQAIPQCSPKDIVNMLNEIFRKLDRIVVIRGVYKVETVSDSYMAVSGIPDYTPE 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNLQLEANNEQLETMTRELELERQKTDSILKDMLPRRIAQQLLSGEHIEACE-HEATVMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLKGQMMLLASKKHIIYLCSPYVTSINELMQYGMRLTAMPLHDATRDLİLLNQQRLSDVE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIPLDFENICNFINAVFVLQVKTSPLKKKHMDAMSQEELKQEMETLDEDATNELTQGHHL
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                                                                                                                                                                                                                                                                                                                                                                                          ASQMESIGMAGKIQCSKWAYQKAMETGRFEFSPRGR 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAENMCHVALGMMWEARSVIDPVSKTPFLLRIGIHSGTITAGVVGTVHPKYCLFGETVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDIVGETAICSQCSPLQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGLHKESDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVDDTLGISLDDFSKALPYHFVIDESCKLVQCGSELHNHIPNELLQPGTPILRIFEINRP
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                 to guanylate
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               cyclase
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Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 240;
                                                                                                                                                                                                                         Consortium.
                                                                                                                                                                                                                                                            10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RWDNSVKKSSRVMD------
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                                 PID:g2702405;
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                                 GSPDB:GN00022;
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                                  CESP: C54E4
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A;Gene: C54E4.3 A;Map position: 4

Ş 멍 δÃ 멍 Ş 밁 Ş 밁 ρ 밁 ğ 밁 Ş 밁 Q 밁 Š 밁 Š Query Match Matches 139; ocal 619 458 338 338 578 S 578 518 560 500 398 451 391 278 222 282 167 241 107 122 AVAAGVPVEVIKESLGE-EVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHCQEAG 181 KRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCF 50 Similarity S 619 AKQVVVPKLERSVRLRIGVHCGPVVAGIVSQQKPRFCVLGNTVNVTKSICSHSSPGKVLV SDEVMSPHGE-PIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINV
: :|: | | | :::|||:| | | | |:| TEIITVVTDLFHRFDRIIEKHKGYKVLSLMDSYLIVGGVPNANQYHCEDSLNLALGLLFE DRLLFEFVPPVIAEALRAAKTVPALMQKRISIDFSEEFSDCSVIFTDIPDFFTISVNCSP VDLLCSIFPCEVAQQLWQGQVVQA------KKFSNVTMLFSDIVGFTAICSQCSP EDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKT ERRKSGMVE--HVIFSVEPDDNHRKGKRLFHKFRNTKTTENAPSFTLS---STILVGLRD LQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMEL VLSYLNTLFIFQLKHHSKRNEVQEGSSEAFQQPLVLKGEMMPINDGNSIIFICSPHVTTV IMTMLNMQFVVRVRRWD--NSVKKSS-----RVMDLKGQMIYIVESSAILFLGSPCVDRL FKNIFPYHVCFNKQMIIEHIGIYLLREYGLENKKTLK----VSDLMQLVQPSDIQLTYKN FCKTFPFHFMFDKDMTILQFGNGIRR---LMNRRDFQGKPNFEEYFEILTPK-INQTFSG HNDCSEFVNQPYLLYSVH-------MKSTK-----PSLSPSKPQSSLVIPTSL FKSEMKGPTFQCEPFGESGLKLHYFSFRQGLFPIVKGLVRKTARTLFEMDVKVCMLERNQ RDILNIKLYISDMPMHDATRDLYMLNQSRICQMELNKKLEETMKKMKKMTEELEVKKSQT ATVLGLSVDDMWEMYGEFLITHACETGWQKMLFCMANNLQEFLDNLNSM---HYFIDQIA Conservative 13.7%; 25.7%; 129; Score 493.5; DB 2 Pred. No. 1.8e-26; Mismatches 218; ۲, Length Indels 583; 55; 180 618 517 499 450 577 559 457 397 337 277 221 281 240 106 13;

Search completed: June 27, 2003, 13:05:23 Job time: 21.5034 secs

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OM protein - protein search, using sw model
                                                                                GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: June 27, 2003, 13:00:58; Search time 34.7899 Seconds
(without alignments)
4086.601 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-762-767A-2 3593 1 MFCTKLKDLKITGECPFSLL.....QKKDVEDGNANFLGKASGID 690

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues

Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : sp_archea:*
sp_bacteria:*

sp_organelle:*
sp_phage:* p_mhc:* 3p_mammal:*

sp_invertebrate:*

sp_plant:*
sp_rodent:*
sp_virus:*

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	. UI	4	w	2	L	Result
781	781.5	784.5	785.5	788	823	985.5	991.5	1097	2005	2009.5	2014.5	2954	3265.5	3266.5	3587	Score
21.7	21.8	21.8	21.9	21.9	22.9	27.4	27.6	30.5	55.8	55.9	56.1	82.2	90.9	90.9	99.8	Query Match Length
614	620	742	600 5	617 1	220 1	676	676	699 :	675]	678 1	678 1	564 4	691 1	691 1	690 4	ength DB
13 P79998	11 054865	11 Q91жJ7	5 077106	13 Q90VY5	11 Q8R5L4	5 Q95SQ4	5 024085	5 077105	13 Q90VV5	13 P79997	13 Q9PWI2	4 Q9NNW8	11 Q9ERL9	11 Q9DBQ3	4 Q8TAH3	B ID
	054865 mus musculu	Q91xj7 rattus norv	077106 manduca sex	Q90vy5 fugu rubrip	Q8r514 rattus norv	Q95sq4 drosophila	Q24085 drosophila	077105 manduca sex	Q90vv5 fugu rubrip	P79997 oryzias lat	Q9pwi2 oryzias lat	Q9nnw8 homo sapien	Q9erl9 mus musculu	Q9dbq3 mus musculu	Q8tah3 homo sapien	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17
452	453	453.5	454.5	455.5	456.5	460	460	461	462	463.5	473	477	478	479	493.5	547	551.5	555	582.5	587	642.5	661	720.5	743	743	749.5	750.5	771.5
12.6	12.6	12.6	12.6	12	12	12.8	12	12	12	12.9			13.3	13.3	13.7	15.2	15.3	15.4	16.2	16.3	17.9	18.4	20.1	20.7	20.7	20.9	20.9	21.5
1100	1076	210	1057	1056	1172	618	344	1112	1076	1057	1055	1055	1276	1047	583	684	699	752	686	685	690	940	649	787	758	751	604	636
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054884	Q9VF19	Q9NH71	Q91x04	Q9YI17	Q9VU79	Q8TA93	Q8R1P8	Q9GT36	Q9W2P1	Q18331	Q98UI1	Q9YGW3	Q8T8L6	Q9PWH0	044468	Q9BI80	Q17707	Q22301	P92006	Q9XTE0	Q9VFC5	076340	Q17010	Q9VA09	Q24086	002298	Q95NK5	Q920Q1
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ALIGNMENTS

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д О	₽ 24	д 9	Db Qy	Ma Be	SORERCE	SEPPE SOOS	RESULT Q8TAH3 ID Q
181 KRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMPPCF 240 	121 QAVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLKOSSHCOEAG 180 	61 QRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSLEREDFEKTIAE 120 	1 MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATVPTCQDIPEKNIQESLP 60 	Query Match 99.8%; Score 3587; DB 4; Length 690; Best Local Similarity 99.7%; Pred. No. 1.6e-272; Matches 688; Conservative 2; Mismatches 0; Indels 0; Gaps	SEQUENCE FROM N.A. TISSUE-BRAIN; TISSUE-BRAIN; Strausberg R.; Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC028384; AAH28384.1; SEQUENCE 690 AA; 77470 MW; D9B98FC0E4DBB927 CRC64;	Q8TAH3; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to guanylate cyclase 1, soluble, alpha 3. Homo sapiens (Human). Eŭkaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	ILT 1 H3 Q8TAH3 PRELIMINARY; PRT; 690 AA.
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XX MEDLINE-21085660; PubMed-11217851;

XX Alawa K., Itawa M., Shlbata K., Yoshino M., Itoh M., Ishii Y.,

XX Alawa K., Itawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

XX Alawa K., Itawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

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XX Radota K., Matsuda T., Nikaido I., Pesole G., Quackenbush J.,

XX Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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XX Radota K., Nilla D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

XX Radota K., Mang K.H., Waldota K., Kamiya M., Lee N.H.,

XX Radota K., Mang K.H., Waldota K., Kamiya M., Lee N
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"Functional annotation of a fi
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EMBL; AK004815; BAB23586.1; -
HSSP; P19687; lAWN.
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Q9DBQ3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                       full-length
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Last sequence up
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Q9ERL9; Q9ERL9; 01-MAR-2001 01-MAR-2001 01-MAR-2002 Soluble guany

PRELIMINARY;

PRT;

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2001 (TrEMBLrel. 16, Created)
2001 (TrEMBLrel. 16, Last sequence guanylyl cyclase alpha 1 sub

: sequence up : annotation ! subunit.

update)

Mus GUCY1A3.

musculus (Mouse) aryota; Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

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Interpro; Ipr002154; G_cyclase.
Pfam; pF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
SMART; SM000452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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                                                                                                              HHQGPNSKPWFQDKDVEDGNANFLGKASGID
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GUANYLATE_CYCLASES_2;
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Pred. No. 2.1e
36; Mismatches
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SEQUENCE
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NCBI_TaxID=10090;
[1]
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InterPro; IPRO01054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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HHQGPNSKPWFQDKDVEDGNANFLGKASGVD
          -QQGTNSKPCFQKKDVEDGNANFLGKASGID
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Pred. No. 2.5
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Zhou Y.H.;

Zhou Y.H.;

Submitted (FEB-2000) to the ELEMBL; AF233750; AAF64043.1; JEMBL; AF233746; AAF64043.1; JEMBL; AF233747; AAF64043.1; JEMBL; AF233749; AAF64043.1; JEMBL; AAF640443.1; JEMBL; AAF640443.1; JEMBL; AAF640443.1; JEMBL; AAF6404454444
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SEQUENCE
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MEDLINE-20183694; PubMed=10717483;
Zhou Y.H., Zheng J.B., Gu X., Li W.H., Saunders G.F.;

"A novel Pax-6 binding site in rodent B1 repetitive elements:
"Coevolution between developmental regulation and repeated ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 20, Last sequence)
01-MAR-2002 (TrEMBLrel. 20, Last annotat
Soluble guanylate cyclase large subunit
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhini
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SMART;
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PS50125;
                                     KGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLK
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                                                                                                                                                       KRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSD
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                                                                                                                                                                                                                                                                                                                RLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKSSRVMDL
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VQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANK
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564 AA;
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GUANYLATE_CYCLASES_2;
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63406 MW;
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"Tandem organization of medaka fish soluble guand betal subunit genes. Implications for coordinate two subunit genes."

J. Biol. Chem. 274:18567-18573(1999).

EMBL; AB022280; BAA76690.1; -.
Interpro-
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Oryzlas latipes (Medaka fish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
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Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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01-MAY-1997
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SEQUENCE
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Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCc; 1.

SMART; SM00452; GUANYLATE_CYCLASES_1;

PROSITE; PS00452; GUANYLATE_CYCLASES_2;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guanylyl cyclase alpha subunit (EC 4.6.1.2).
Cryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzias.
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HSSP; P19687; 1AWN
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Mikami T., Kusakabe T., Suzuki N.;
Molecular cloning of cDNAs and expression
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B000849; BAA19198.1; -.
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                                                                                                    Query Ma
Best Loc
Matches
                                                                                                                                                                Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;

I "Identification of tandem organization of soluble guanylyl cyc
I alphal and betal subunit genes in the Japanese pufferfish (Fug
I rubripes) genome.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB062171; BAB60907.1; -.

R EMBL; AB06219; BAB60907.1; -.

R EMBL; AB06219; BAB60905.1; -.

R InterPro; IPR001054; G_cyclase.

R Pfam; PF00211; guanylate_cyc: 1.

R Pfoam; PF00211; guanylate_cyc: 1.

R PROSITE; PS00125; GUANYLATE_CYCLASES_1; UNKNOWN_1.

R PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

SEQUENCE 675 AA; 75498 MW; E71A283DC0369601 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Soluble guanylyl cyclase alphal subunit.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Morinaga C., Yamam
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Pred. No. 1.6e
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pfam; pF00211; guanylate_cyc; 1.
smarr; sm00044; CYCc; 1.
proSITE; pS00452; GUANYLATE_CYCLA.
proSITE; pS50125; GUANYLATE_CYCLA.
                                                                                                                                                                                                                                                                                                                                                                                                                      077105
077105;
                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
501uble guanylyl cyclase alpha-1 subunit.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glos Sphingiodea; Sphingidae; Sphingidae; Manduca.
NCBI_TaxID-7130;
                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98409773; PubMed-9736646;
Nighorn A., Gibson N.J., Rivers D.N.
"The nitric oxide-cCMP pathway may
sensory afferents and projection ne
manduca sexta.";
                                                                                              J. Neurosci. 18:7244-7255(1998).
EMBL; AF062750; AAC61263.1; -.
HSSP; P19687; 1AWN.
                                                                                                                                                   manduca sexta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDDPEHFVKMMSMFSSRKAIQMDTLRVALGEELFNMCYEEDRHILRVVGGALHDFLNSFN
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                                                                                687; 1AWN.
IPR001054;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
               GUANYLATE_CYCLASES_1;
GUANYLATE_CYCLASES_2;
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Glossata; Ditrysia;
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650 644 590 530 524 470 464 410

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Best Local
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                                                                                                            Q24085;
01-NOV-1996 (TremBirel. 01, Created)
01-NOV-1996 (TremBirel. 01, Last sequence update
01-MAR-2002 (TremBirel. 20, Last annotation upda
GYCALPHA99B protein.
GYC-ALPHA-99B OR GYCALPHA99B OR DGCA1 OR CG1912.
                                                             Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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SEQUENCE
    SEQUENCE FROM N.A. STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA-GVPVEVIKESLGEEVFKICYEED---ENILGVVGGTLKDFLNSFSTLLKQSSHCQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPF-----SLLAPGQVPNESSEEAAGSSESCKATVPICQD-----IPEKNIQESLPQRK
                                                                                                                                                                                                                                                                       FPKDIHGTCYFLHKYTHPGTDPGEP--QVKHIREALKDYGIGQANSTD
                                                                                                                                                                                                                                                                                      FPSEIPGICHFLDAY-QQGTN-SKPCFQKKDVEDGNANF-LGKASGID
                                                                                                                                                                                                                                                                                                                              VVGKTMLKYCLFGHNVTLANKFESGSEPLKINVSPTTYEWLIKFPGFDMEPRDRSCLPNS
                                                                                                                                                                                                                                                                                                                                              VVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWQGQVVQAKKFSNVTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMFCLKMPGSTALAEG--LEIKGQMVFCAESDSLLFVGSPFLDGLEGLTGRGLFISDIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-KRGRLE-DASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATDSVNTKDFMAKLGEVILLTAFSHNCRLERAFKCLGTNLTEFLTTLDS-VHDVLHDQDT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPSNECLHAAVTSLTKNQSDHYHKYN------CLRRLPDDVKTCRNYAYLQEIYDAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPFRRASSQHQFANGGSSAPKKPEFRSRTSSVHLTGPEEEDGERNTLTLKHMSEAL-QLL
                                                                                                                                                                                                                                                                                                                                                                                                                                           LWIGEKIEAKSHDDVTMLFSDIVGFTSICATATPMMVIAMLEDLYSVFDIFCEELDVYKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWHFITDKRLELVQLGAGFMRLFGTHLATHGSSLGTYFRLLRPRGVPLDFREILKRVNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNFEEYFEILTPK-INQTFSGIMTMLNMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SYTNDPRRF---RYEINAVPLHQKSKEDSCELVNEAASVATSTKVTDLKIGVASFCKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCFHNDCSEFVNQPYLLYSV--HMKSTK-----PSLSPSKPQSSLVIPTSLFCKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLKDETMEYEANFVCTTSQEGKIQLHLTTESEPVAYLLVGSLKAIAKRLYDTQTDIRLR-
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                                                                                                                                                                                                    PRELIMINARY;
                                                         Drosophilidae;
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Last sequence update)
Last annotation update)
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Pred. No. 2.5e
30; Mismatches
                                                                                                                                                                                                    PRT;
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Goong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Goong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A., RA Melson D.R., Milshina N.V., Mobarry C., Morris J., McShrefi A., RA Ra Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Shao Q., Zheng L., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., RTAN S., Yeb R.-F., Zaveri J.S., Zhan M., Zhang G., Zha Q.A., Shan M., Zhang G., Zha Q.A., Shan M., Zhang G., Zha Q.A., Shan M., Shan M., Zhang G., Zha Q.A., Shan P., Shan M., Zhang G., Zha Q.A., Shan M., Shan M., Zhang G., Zha Q.A., Shi Chan M., Zhang G., Zhu X., Smith H.O., Ran Rainer G., Shan M., Zhang G., Zhu X., Smith H.O., Ran Rainer G., Shan M., Zhang G., Zhu X., Smith H.O., Ran Rainer G., Shan M., Zhang G., Zhu X., Smith H.O., Ran Rain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Chandra I.,
Chamber M., Dough L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Ra Cherry J.M., Cawley S., Dahlke C., Borers R., Bristonmann W.
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain soluble guanylyl cyclase.";
J. Biol. Chem. 270:15368-1376(1995).
EMBL; AE003770; AAP56917.1; -.
EMBL; U27117; AAAB7940.1; -.
HSSP; P19687; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0013972; Gyc-alpha-99B InterPro; IPR001054; G_cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=OREGON-R;
MEDLINE=95318108; PubMed=7797526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 676 AA; 75662 MW; CE8097E1EC3787F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two Drosophila genes that encode the brain soluble guanylyl cyclase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shah S., Hyde D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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      142
                                                         160 KDFLNSFS---TLLKQSSHCQEAGKRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILP
                                                                                                                      87
                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
QEFLGSLDGVYDVLK----LQEED----VTDTGFVCAGEGE----LIFTSERPVIAWLLL
                                                                                                                                                                         KSLEREDFEKTIAE-----QAVAAGVPVEVIKESLGEEVFKICYEE-DENILGVVGGTL
                                                                                                                                                                                                                                                                                            SLPQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAK------HKIK---ESR
                                                                                                                   KSCANYDYLADIQELLLKMDEASASEILV-----LLGEELITCCCTGIIERAFRCLGTDL
                                                                                                                                                                                                                                      ALEDEELSDDALTLTHLQMAIQLLTAPSNEDLNTAVTSLVAKYRQNWPNIHKLKLDPQTF
                                                                                                                                                                                                                                                                                                                                                         Conservative 117;
                                                                                                                                                                                                                                                                                                                                                                                    27.6%;
37.8%;
                                                                                                                                                                                                                                                                                                                                                                                 Score 991.5;
Pred. No. 4.4
                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Query Match
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EMBL; AY060654; AALZ8202.1; -.

EMBL; AY060654; AALZ8202.1; -.

FlyBase; FBgn0013972; Gyc-alpha-99B.
InterPro; IPR001054; G_Cyclase.
Pfam; PF00211; guanylate_cyc; 1.

PROSITE; PS50125; GGANYLATE_CYCLASES_2; 1.

PROSITE; PS50125; GGANYLATE_CYCLASES_2; 1.
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01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
Stapleton "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q95SQ4
Q95SQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYC-ALPHA-99B OR GYCALPHA99B OR CG1912.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hererygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
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1 (TrEMBLrel.
2 (TrEMBLrel.
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Last sequence update)
Last annotation updat
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Pred. No. 1.3e-68;
7; Mismatches 210;
  -QAVAAGVPVEVIKESLGEEEVFKICYEE-DENILGVVGGTL
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Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Soluble guanylate cyclase alpha2d (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalla; Eutheria; Rodentia; Sciurognathi; Muric
                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                 Okamoto H., Asakawa T.;
"Molecular cloning of a novel variant of the cyclase beta2 subunit.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; AB079780; BAB84824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
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Best Local S
Matches 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00211; guanylate_cyc; 1.

PROSITE; PS00132; CARBOXYPEPT_ZN_1; UNKNOWN_1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

SEQUENCE 617 AA; 70236 MW; 7B531B5896A06191 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alphal and betal subunit genes in the Japanese pufferfis rubripes) genome.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062170; BAB60908.1;
EMBL; AB062170; BAB60906.1;
InterPro; IPR001054; G_cyclase.
InterPro; IPR000834; Zn_carbOpept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygil; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morinaga C., Yamamoto T.,
"Identification of tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRGCS-BETA1.
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  QMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKR
                                                                                                                                                                                 FYEDLDGFEENGTQETRISPYT-FCKAFPFHLMFDRDLMLTQCGNAIYRVLPQLQ-PGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KESRKSLEREDFEKTIAEQA-----VAAG-----VPVEVIKESLGEEVFKICYEED-ENI
                                                                             ILPSVFSLVRPHIDFSFHGILSHINTVFVLRSKEGLLNVETVENEDELTGVEISCLRLKG
                                                                                                                                NFEEYFEILTPKINQTFSGIMTMLNMQFVVR-----VRRWDNSVKKSSRVMDLKG
                                                                                                                                                                                                                                                                                                                                                                                             LRVLGSNVREFLQNLDAL-----HDHLGTIYPGMRAPSFRCTDAEKGNSLILHYYSEREG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REAQLDIEGQFLVRIIYEDAKTYDLVAAASKVLKIDAGDILQLFGKMFFEFCQESGYDTI
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(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 20, Last annotation
nylyl cyclase betal subunit.
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                                                                                                                                                                                                              -PSLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKP
: | : | : | | | | | | | | | | : : : | | | | | | | : : : |
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n organization of soluble guanylyl cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 788; DB 13;
Pred. No. 3.5e-53;
2; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7B531B5896A06191 CRC64;
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Best Local 9
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077106;
01-NOV-1998
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01-NOV-1998 (TIEMBLIEL 08, Last sequence update)
01-MAR-2002 (TIEMBLIEL 20, Last annotation update)
901-MAR-2002 (TIEMBLIEL 20, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nighorn A., Gibson N.J., Rivers D.M., Hildel "The nitric oxide-cGMP pathway may mediate c sensory afferents and projection neurons in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   manduca sexta.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Neurosci. 18:7244-7255(1998).
EMBL; AF062751; AAC61264.1; -.
HSSP; P16068; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-98409773; PubMed-9736646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase
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                                                                                                                                                                                                                                                                                                                                                             131 VIKESLGEEVFKICYEED-ENILGVVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDAS
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VQAGRTVSRLLPRVTRPG-CKITDVLDTVRPHLEMTFANVLAHINTVYVLKTKPEEMSVT
                                                LQFGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSV-
                                                                                              TETSTTGRVSAPEIA-EIETLSLEPKVSP--
                                                                                                                                                                                                    GFTAICSQCS----PLQVITMLNALYTREDQQCGELD----VYKVETIGDAYCVAGGLHKE
                                                                                                                                                                                                                                                                                                               AILELFGKTFFEFCQDSGYDKILQVLGATPRDFLQNLDGL-----HDHLGTLYPGMRSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 AA; 68099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 106;
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                                                                                                                                                 -VNQPYLLYSVHMKSTKPSLSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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Best Local S
Matches 194
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in the Absence of a Second Subunit.";
J. Biol. Chem. 276:30737-30743(2001).
EMBL; AY004153; AAF86581.1;
InterPro: IPRONIUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91XJ7
Q91XJ7;
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InterPro; IPR0010230; Prenyl_site.
Pfam; PF00211; guanylate_cyc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_1.
PROSITE; PS0125; GUANYLATE_CYCLASES_2; UNKNOWN_1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 742 AA; 83050 MW; 41CE148B15E244E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2002 (TrEMBLrel. 20, La
Soluble guanylyl cyclase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic organization of alpha soluble guanylyl cyclase genes. Proc. Natl. Acad. Sci. U.S.A. 9 EMBL; AF020339; AAB94875.1; -. EMBL; AF297083; AAG17447.1; -. HSSP; P16068; IAWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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rPro; IPR001054; G_cyclase.
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PS50125;
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GUANYLATE_CYCLASES_2;
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Rodentia;
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06, Last sequence update)
20, Last annotation update)
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EMBL/GenBank/DDBJ
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Pred. No. 1.
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Sciurognathi;
HDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGLQ
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604 550	544 491	491 431	431 371	371 311	321 251	266 193	213 144
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Search completed: June 27, 2003, 13:04:41 Job time: 38.7899 secs

Title: Perfect score: Sequence:

US-09-762-767A-2 3593

MFCTKLKDLKITGECPFSLL.....

QKKDVEDGNANFLGKASGID

protein

protein search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compugen

June

27,

2003, 13:03:32; Search time 14.2322 Seconds (without alignments)
1426.467 Million cell upda

cell updates/sec

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
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/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Maximum

DB

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length:

2000000000

Total number

of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

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COMPUTER REALIZATION OF TELEPHONE: Floppy disable COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTION NUMBER: US/07/623,033 FILING DATE: 19901206 CLASSIFICATION 1435 ATTORNEY/AGENT INFORMATION: NAME: Kohn, Kenneth I. REGISTRATION NUMBER: UJ/07/623,033 REGISTRATION NUMBER: UJ/07/623,033 FILING DATE: 19901206 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Kohn, Kenneth I. REGISTRATION NUMBER: UJ/01/8 REGERENCE/DOCKET NUMBER: UJ/01/8 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1D NO: 2:
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                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-623-033-2
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US-07-623-033-2
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Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312) 456-800: INFORMATION FOR SEQ ID NO: 22 SEQUENCE CHARACTERISTICS: LENGTH: 1075 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Garbers, David L.
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: CLONING :
NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606-4002
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STREET: 10
                                                                                              764
                                          479 NYTMLESDIVGETAICSQCSPLQVITMLNALYTREDQQCGELDVYKVETIGDAYCVAGGL 538
                                                                                                                       423 DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS
                                                                                                                                                                                                                 Similarity
                                                                                            DTLIRRLQLYSRNLEHLVEERTQLYKAERDRADHLNFMLLPRLVVKSLKEKGIVEPELYE
EVTIYFSDIVGFTTICKYSTPMEVVDMLNDIYKSFDQIVDHHDVYKVETIGDAYVVASGL
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US-09-205-426-178
US-09-205-426-178
US-08-997-080-174
US-08-997-362-174
US-09-92-426-174
US-09-324-542-174
US-09-325-426-174
US-08-857-076-75
US-08-997-080-125
US-08-997-080-125
US-08-997-862-125
US-09-925-855-125
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178, App
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Result

Query Match

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1075 1077 1077 1099 1099 1090 1090 1194 11134 11253 12

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sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

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US-09-412-210-1
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                                                                                                                    Sequence 8, Application US/08726214 Patent No. 6107076 GENERAL INFORMATION:
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TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
FILE REFERENCE: 5800-47
CURRENT APPLICATION NUMBER: US/09/412,210
CURRENT FILING DATE: 1999-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                     APPLICANT: Tang, Wei
APPLICANT: Gilman, A
TITLE OF INVENTION:
TITLE OF INVENTION:
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                         CORRESPONDENCE ADDRESS:
                                      NUMBER OF SEQUENCES:
           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                              HECMRIKILGDCYYCVSGLPLSLPDHAINCVRMGLDMCRAIRKLRAATGVDINMRVGVHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSRPALLPQLAANAVLFLCGNVA------GVY------HKALME------RA---
                                                                                                                                                                                                                                                                   ------PGF-VFTPRSREE 641
                                                                                                                                                                                                                                                                                                                               GSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LRATFREALSSLHSRRRLDTEKKHQEHLLLSILPAYLAREMKAEIMARLQAGQ 251
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                                                  Gilman, Alfred G.
VENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
VENTION: AND USES THEREFOR
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                                                                                                        Tang, Wei-Jen
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          White
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Pred. No. 4.6e-23;
55; Mismatches 98;
        Durkee
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US-08-726-214-14
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                                                                                                                                                                        Sequence 14, Applicat Patent No. 6107076 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (512) 474-757 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                         APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
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APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
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     COUNTRY:
                                                  STREET:
                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                               Houston
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                                           P.O. Box 4433
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United States of
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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31.2%;
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Pred. No. 1e-22;
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RESULT 5
US-08-307-896-3
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                                                                                                            GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
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Matches
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                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELLEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                        CURRENT APPLICATION NUMBER: US/08/307,896C CURRENT FILING DATE: 1994-09-16
                                   NUMBER OF SEQ
SOFTWARE: Fast
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APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ENGTH:
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REGISTRATION NUMBER: 37.642
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                   SEQ ID NOS: 9
FastSEQ for Windows Version 3.0
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                                                                                    TELEFAX: (512) 474-75 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tang, Wel-Jen
APPLICANT: Gilman, Alfred G.
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                STRANDEDNESS:
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                         NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit
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TOPOLOGY:
                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 LYLSDIP-----IHNALRDVVLI--GEQARAQDGLKKRLGKLKATLEQAHQ-----
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). 6107076
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                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                         (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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Pred. No. 2.1e-22;
""amatches 86;
                                                                                                                                                            UTSD:450
                                                                                                                                                                                                                                                                                                   Herewith
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8.98;

Score 319;

DB 3;

Length 1090;

Best Local Similarity

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 Query Match 8.9%;
Best Local Similarity 30.4%;
Matches 80; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application:
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                                                                                                                                                           TELEX: 650 6111063
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino aci
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US OF FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION: NAME: Clark, Richard S.
                                                                                                                                                                                                                                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/307,896
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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STATE:
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                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                            1090 amino acids
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                                                                                                                                                                                           (212) 765-2519
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VENTION: MUTANT ACTIVATED GSALPHA AND
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                                                                                                                                                                                                            (212) 408-2500
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CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
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              Score 319; DB 5; Pred. No. 2.1e-22;
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                                                                                                                                                                                                                                         29970 165/28755
 Mismatches
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 96;
                             Length 1090;
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44;
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US-08-726-214-6
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                                                                                     Query Match
Best Local :
                                                                       Matches
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                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITTLE OF INVENTION: SOLUBLE MANMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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COUNTRY: 77210
                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                          TELEFAX:
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                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                    NAME: Highlander, St
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/005,498 FILING DATE: 04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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433 KATLE-----QAHQALEEEKKKTVDLLCSIFPCEVAQQL-------WQGQVVQA 474
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                                                                                     Similarity
                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                      1144 amino acids
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                                                                      Conservative
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                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0,
                                                                                                                                                                                                                                                                       (512) 418-3000
                                                                  8.4%; Score 303; DB 3; 30.7%; Pred. No. 8.8e-21; ative 50; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                     Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND USES THEREFOR
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                                                                                                   Length 1144;
                                                                  Indels
                                                                  48;
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                                                                  Gaps
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US-08-726-214-2
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Patent No. (
                                                                                                                                     Matches
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                  TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/726,214
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 6
FILING DATE: 04-OCT-1995
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APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE:
TITLE OF INVENTION: AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                                                                   amino acid
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AGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRY 594
                                LEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQG------QVVQAKKFSNVTMLFSD 486
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28.1%;
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                                                                                                                                 Score 302; DB 3; 1
Pred. No. 1.1e-20;
7; Mismatches 94;
                                                                 ---VNVYGIF--VRILAERAQRKAFLQAR----N 250
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US-08-726-214:18
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Best Local
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
Arnold, White & Durkee
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APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                               554 LKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLEGNNVTLANKFESCSVP 613
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 LDMIDTITSVAEATEVDLNMRVGLHTGRVLCGVLGLRKWQYDVWSNDVTLANVMEAAGLP
                                                              ASQCTAQELVKLLNELFGKFDELATENHCRRIKILGDCYYCVSGLTQPKTDHAHCCVEMG 142
                                                                                                                                                              LEEEKKKTVDLLCSIFPCEVAQQLWQG-----QVVQAKKFSNVTMLFSDIVGFTAI 493
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                                                                                                                                                                                              8.3%; Score 299.5; DB 3; 32.6%; Pred. No. 5.5e-21; tive 44; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               37,642
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US-08-726-214-16
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-864-785-2
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 1253
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APPLICANT: Kaplan, Joshua
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CURRENT APPLICATION NUMBER: US/08/864,785A

CURRENT FILING DATE: 1997-05-29
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APPLICANT: Hart, Anne C.
                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE |
TITLE OF INVENTION: AND USES
NUMBER OF SEQUENCES: 31
                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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               APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewit
CLASSIFICATION:
                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                      United States of America
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               Concurrently Herewith
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Pred. No. 3.0
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                                                                      Version
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RESULT 13 US-08-726-214-10

Sequence 10, Application Patent No. 6107076 GENERAL INFORMATION:

US/08726214

APPLICANT:

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Wei-Jen

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TOPOLOGY:
US-08-726-214-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 6:
FILING DATE: 04-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Highlander, Steven L.
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VIGAKKPQYDIWGKTVNLASRMDSTGVSGRIQVPEETYLILKD-QGFAFDYR 1147
                                 VVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPR 637
                                                                                                                                                                                 NVTMLFSDIVGFTAICSQC----SPLQVITMLNALYTRFDQQCGE---LDVYKVETIGDA 531
                                                                                                                                                                                                                      EYTARLDFLWRVQAKEEINEMKDLREHNENMLRNILPGHVARHFLEKDRDNEELYSQSYD
                                                                                                                                                                                                                                                    KLKATLE-----QAHQALEEEK---KKTVDLLCSIFPCEVAQQLWQ-----GQVVQAKKFS
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                                                                       YMAVSGLSPEKQQCEDKWGHLCALADFSLALTESIQEINKHSFNNFELRIGISHGSVVAG
                                                                                                         YCVAGGLHKESDT-----HAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAG 585
                                                                                                                                               AVGVMFASIPGFADFYSQTEMNNQGVECLRLLNEIIADFDELLGEDRFQDIEKIKTIGST 1036
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                                                                   RESULT 14
US-09-008-097-4
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             Sequence 4, Application US/09008097 Patent No. 6306830 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: //210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PAtentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acid
     APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 7.9%; So
1 Similarity 26.4%; Pi
83; Conservative 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAHQALEEEKKKTVDLLCSIFPCEVAQQL------WQGQVVQAKKFSNVTMLFSDI
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                                                                                                                                                                                                                                                                                                                                   CCVEMGMDMIEAISSVREVTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHM 432
                                                                                                                                                                                                                                                                                                                                                                   QIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKF 607
                                                                                                                                                                                                                                                                                                                                                                                                    EGFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLPEARADHAH 372
                                                                                                                                     ANPEDEVDEFLGRA 560
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                                                                                                                                                                                                                                                                   EAGGKAGRIHITKATLNYLNGDYEVEPGCGGERNAYLKEHSIETFLILRCTQKRKEEKAM
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   Hammond, H. Kirk
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Pred. No. 7.1e-19;
52; Mismatches 108;
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US-09-008-097-6
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                                             Sequence 6, Application US/09008097 Patent No. 6306830 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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US-09-008-097-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
FRAGMENT TYPE:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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ZIP: 94304-1018
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                                                                                                                                175 GFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLPEARADHAHC
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                                                                                                                                                                                                115 QARLHIQHENRQQERLLISVLPQHVAMEMKEDINTKKEDMFHKIYIQKHDNVSILFADIE 174
 295
                             609 SCSVPRKINVSPITYRLL 626
                                                                                                                                                                                                                              438 QAHQALEEEKKKTVDLLCSIFPCEVAQQLWQG-----QVVQAKKESNVTMLFSDIV
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                                                                CVEMGVDMIEAISLVREVTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHME
AGSRAGRIHITRATLQYL 312
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                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 3.3e-19;
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Hammond, H. Kirk Insel, Paul A. Ping, Peipei

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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
; FRAGMENT TYPE: inter
US-09-008-097-6
Search completed: June 27, 2003, 13:05:57 Job time: 16.2322 secs
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Best Local Similarity
Matches 63; Conserv
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
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NAME: Dylan, Tyler M
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 2200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Post, Steven R.
APPLICANT: Gao, Meihua
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
TITLE OF INVENTION: HEART FAILURE
UNDBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CTIT: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                            506 AGSRAGRIHITRATLQYL 523
                                                                                                                       609
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                                                                                                                                                                                                                                386 GFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLPEARADHAHC 445
                                                                                                                                                                                                                                                                           489
                                                                                                                                                                                                                                                                                                             326 QARLHIQHENRQQERLLLSVLPQHVAMEMKEDINTKKEDMFHKIYIQKHDNVSILFADIE 385
                                                                                                                                                                                                                                                                                                                                    438 QAHQALEEEKKKTVDLLCSIFPCEVAQQLWQG------QVVQAKKFSNYTMLFSDIV 488
                                                                                                                                                                                                                                                                       GFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHKESDTHAVQ 548
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compuc
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US-10-121-911-1
US-10-282-942-2
US-10-282-942-2
US-09-750-240-4
US-09-750-240-6
US-09-750-240-6
US-09-750-240-11
US-09-750-240-11
US-09-750-240-11
US-09-750-240-13
US-09-751-100B-2
US-10-0751-100B-2
US-09-751-100B-9
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                                                                     Sequence 162, Appli
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	3.7	3.7	3.7	3.7	3.7	ა 8	3.8	3.9	4.1	4.1	4.1	4.1	4.8	5.1	5.2	5.2	5. 3			5.4			5.4-	5.4	5.4	5.8
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AT TOWERED	US-09-751-100B-58	US-09-751-100B-57	US-09-751-100B-56	US-09-751-100B-55	US-09-751-100B-54	US-09-751-100B-61	US-09-751-100B-60	US-09-751-100B-59	US-09-764-869-1060	US-10-091-504-1060	US-09-989-442-143	US-09-764-868-795	US-09-989-442-92	US-09-925-297-515	US-09-880-505-125	US-10-051-643-125	US-09-844-353A-75	US-09-205-658-75	US-09-844-353A-76	US-09-205-658-76	US-09-915-582-50	US-09-880-505-174	US-10-051-643-174	US-09-880-505-178	US-10-051-643-178	US-09-989-442-141
	-	Sequence 57, Appl	56,	•	54,	61,	Sequence 60, Appl	Sequence 59, Appl	æ	Sequence 1060, Ap	143	Sequence 795, App	Sequence 92, Appl	Sequence 515, App	125	125	75,	75,	76,		•	174,	174,	Sequence 178, App	Sequence 178, App	Sequence 141, App

ALIGNMENTS

US-10-205-823-162

GENERAL INFORMATION

APPLICANT: Schlegel, Robert APPLICANT: Monahan, John E

APPLICANT:

APPLICANT:

Monahan, John E. Endege, Wilson O. Gannavarapu, Manjula Gorbatcheva, Bella

APPLICANT:

APPLICANT: APPLICANT:

Hoersch, Sebastian Kamatkar, Shubhangi Wonsey, Angela M. Glatt, Karen Sequence 162, Application US/10205823 Publication No. US20030108963A1

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; ORGANISM: Homo sapiens US-10-205-823-162
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILLING DATE: 2001-07-25
PRIOR FILLING DATE: 2001-08-22
PRIOR FILLING DATE: 2001-08-22
PRIOR PELICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 50/341,746
PRIOR APPLICATION NUMBER: 50/341,746
PRIOR APPLICATION NUMBER: 50/341,746
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 162
LENGTH: 690
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: MRI-044
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Zhao, Xumei
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100.0%;
Score 3593; DB 9; Pred. No. 1e-305;
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                    TYPE: PRT
ORGANISM: Mus :
S-09-952-213D-2
                                                                                                                                                          Sequence 2, Application US/09952213D Publication No. US20030096240A1 GENERAL INFORMATION:
 Query Match
                                                        SEQ
                                                                                                         APPLICANT: MURAD, FERID
APPLICANT: SHARINA, IRAIDA G.
APPLICANT: KRUMENACKER, J. S.
APPLICANT: MARTIN, E.
APPLICANT: MARTIN, E.
TITLE OF INVENTION: GENOMIC ORGANIZATION OF MOUSE
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                                                       CURRENT APPLICATION NUMBER: US/09/952,213D CURRENT FILING DATE: 2002-08-16 NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                    FILE REFERENCE: UTSH: 252US
                                                LENGTH: 691
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RESULT 3
US-10-157-031-18
; Sequence 18, Application US/101:
publication No. US20030108890A1
; GENERAL INFORMATION:
; ORGANISM: Homo US-10-157-031-18
                                                                                                APPLICANT: KOZIOV, ... APPLICANT: LObashev, A. V.
APPLICANT: Krukovskaya, L. L.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening
PEPERENCE: 2760-103
PEPERENCE: 2760-103
                                     SEQ ID NO 18
LENGTH: 1073
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                                                                 FILE REFERENCE: 2760-103

CURRENT APPLICATION NUMBER: US/10/157,031

CURRENT FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 415

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                            APPLICANT: Baranova, A. V. APPLICANT: Yankovsky, N.
           TYPE: PRT
ORGANISM:
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                                                                                                                                                               Baranova, ...
Yankovsky, N. K.
Kozlov, A. P.
Kozlov, A. V.
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-249-2
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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Best Local Similarity
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods For Identifying And Targeting Cancer Cel
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TJU2412
CURRENT APPLICATION NUMBER: US/09/819,249
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Waldman, Scott A. APPLICANT: Park, Jason APPLICANT: Schulz, Stephani
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                                                                                                                                                                                                                  HKES-DTHAVQIALMALKMMELSDEVMSPH--GEPIKMRIGLHSGSVFAGVVGVKMPRYC
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                                                                                                                                                                              PKRNGNRHAIDIAKMALEILSFMGTFELEHLPGLPIWIRIGVHSGPCAAGVVGIKMPRYC
                                                         FL----DAYQQGTNSKPCFQKKDVEDGNAN 681
                                                                                                LFGDTVNTASRMESTGLPLRIHVSGSTIAILK--
                      FLYEVRGETYLKGRGNETTYWLTGMKDQKFN 1009
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37.3%;
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37.3%;
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Pred. No. 1.2e-26;
43; Mismatches 92;
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Pred. No. 1.2e-26;
Pred. No. 1.2e-26;
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; ORGANISM: Homo
US-10-282-942-2
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US-10-282-942-2
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Patent NO. US20020164632A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 21529, A NOVEL ADENVLATE CYCLASE
FILE REFERENCE: 5800-47
FILE REFERENCE: 5800-47
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LENGTH: 1077
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10282942 Publication No. US20030087295A1 GENERAL INFORMATION:
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Query Match
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                                                                                                                                     SEQ ID NO 2
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CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/335,047
PRIOR FILING DATE: 2001-10-31
                                                                                                                                                                                                                                                                      APPLICANT: Silos-Santiago, Inmaculada TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: TREATMENT AND DIAGNOSIS FILE REFERENCE: MPIOI-240P1RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/412,210 PRIOR FILING DATE: 1999-10-05 NUMBER OF SEQ ID NOS: 2
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CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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                                                                                                                                                         SOFTWARE: FastSEQ
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8.8%;
28.2%;
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  316; DB 9;
No. 1.5e-18;
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                  Length 1080;
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; NAME/KEY: SITE
; LOCATION: (829)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 811
LENGTH: 855
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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LOCATION: (479)
OTHER INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                     433 KATLE-----QAHQALEEEKKKTVDLLCSIFPCEVAQQL-------WQGQVVQA 474
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                                                                                                                         ICGLPDYREDHAVCSILMGLAMVEAISYVREKTKTGVDMRVGVHTGTVLGGVLGQKRWQY 186
                                                                                                                                                              AGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRY 594
                                                                                                                                                                                                            YRHENVSILFADIVGFTQLSSACSAQELVKLLNELFARFDKLAAKYHQLRIKILGDCYYC 126
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Pred. No. 1.3e-17;
2; Mismatches 93;
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                                                                                                                                                                                                          US-09-750-240-6
Sequence 6, Application US/09750240
Patent No. US20020103147A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-750-240-4
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US-09-750-240-4
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SEQ ID NO 4
LENGTH: 604
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Best Local :
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                            APPLICANT: POST, S. R.
APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
FILE REFERENCE: 2200020556723
FILE REFERENCE: 220002056726
  CURRENT FILING
                                                                                                                                                              APPLICANT: Hammon, H. K. APPLICANT: Insel, P. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
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                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
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Local Similarity 31.8%;
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APPLICATION NUMBER: US/09/750,240 FILING DATE: 2001-10-12
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                                                                                                                       Ping, P.
Post, S. R.
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Q for Windows Version 4.0
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Pred. No. 5.3e-16;
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; ORGANISM: human type V adenylyl cyclase
US-10-175-158-2
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                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1261
                                                                         Query Match
Best Local Similarity
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Publication No. US20030008371A1
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Best Local Similarity 31.8%;
Matches 63; Conservative 4
                                                          Matches
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APPLICANT: Cor Therapeutics, Inc.
APPLICANT: Cor Therapeutics, Inc.
TITLE OF INVENTION: CLOUING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5027-01-US
CURRENT FILINGIATION NUMBER: US/10/175,158
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US/09/473,716
PRIOR APPLICATION NUMBER: US/09/473,716
PRIOR APPLICATION NUMBER: US/09/473,716
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PRIOR FILLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILLING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US98/13540 PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1997-07-01
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ORGANISM: Homo sapiens
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FILING DATE: 1998-01-16
APPLICATION NUMBER: US 08/924,757
FILING DATE: 1997-09-05
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438 QAHQALEEEKKKTVDLLCSIFPCEVAQQL-------WQGQVVQAKKFSNVTMLFSDI
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                                                          Conservative
                                                      7.8%; Score 280.5; DB 9; 26.4%; Pred. No. 2.4e-15; Live 52; Mismatches 108;
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; TYPE: PRT
; ORGANISM: human type VI adenylyl cyclase
US-10-201-000-2
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Best Local
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PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: PCT/US98/13694
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,904
PRIOR EILING DATE: 1997-07-01
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TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
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SOFTWARE: PatentIn Ve:
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                                               600 NYTLANKFESCSVPRKINVSPTTYRLL
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                                                                                                                                                                                         VSILFADIEGFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLP 437
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DVTLANHMEAGGRAGRIHITRATLOYL
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                                                                                            EARADHAHCCVEMGVDMIEAISLVREVTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSN 497
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                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 279.5; DB 9; 30.4%; Pred. No. 2.6e-15; 47. Mismatches 82;
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Sequence 11, Application UPatent No. US20020103147A1

Application US/09750240

INFORMATION:

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RESULT 13
US-09-750-240-13
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PRIOR FILING DATE: 1999-12-27
PRIOR PELICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
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                FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-77
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                            APPLICANT: Gao, M.
TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
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CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
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APPLICATION NUMBER: US 08/924,757
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                                                                                                                                                                                                                   Ping, P.
Post, S. R.
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30.4%; Pred. No. 2.6e-15
ative 47; Mismatches 8
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                                                                                                                                 ; TYPE: PRT; ORGANISM: human type IX adenylyl cyclase US-10-071-223-2
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                              SEQ ID NO 2
                                                          Matches
                                                                        Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COR Therapeutics, Inc.
APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/071,223
CURRENT FILING DATE: 2002-02-11
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/473,717
PRIOR FILING DATE: 1999-12-29
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1997-06-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Storm, Daniel R.
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                                                                                                                                                                                          LENGTH: 1294
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INFORMATION:
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                                                                                                                                                                                                                               PatentIn
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44481-5029-02-US
                                                                          7.3%;
29.9%;
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                                                        58;
                                                   Score 263.5; DB 1
Pred. No. 7.7e-14;
68; Mismatches 89
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                                                                                            DB 12;
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CURRENT APPLICATION NUMBER: US/09/751,100B
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1353
TYPE: PRT
ORGANISM: Mouse
US-09-751-100B-2
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Search completed: June 27, 2003, 13:17:11 Job time: 37.3713 secs
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US-09-751-100B-2
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Best Local Similarity 29.4:
68; Conservative
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Patent No. US20020142436A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor
FILE REFERENCE: P27948A
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                                                                                                                                                     432 QTKCEKISTLGDCYYCVAGCPEPRAD-HAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGV 490
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                                                                                                HSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKD 628
                                                                                                                                                                              ELDVYKVETIGDA-YCVAGGLHKESDTHAVQIALMALKMMELSDEVMSPHGEPIKMRIGL 577
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                                                                 HTGTVLCGILGMRRFKFDVWSNDVNLANLMEQLGVAGKVHISEATAKYLDD 541
                                                                                                                                                                                                                                     KAPIAFRPFKMQQIE-----EVSILFADIVGFTKMSANKSAHALVGLLNDLFGRFDRLCE 431
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                                                                                                                                                                                                                                                                                                                                                                                            7.3%; Score 260.5; DB 10; 29.4%; Pred. No. 1.5e-13; rative 59; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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ALIGNMENTS

RESULT 1 AAY51608

AAY51608 standard; Protein; 619 AA.

26-MAY-2000 (first entry)

Human soluble guanylylcyclase beta1 protein.

Human; guanylyloyclase alphai; hsGCalphai; hsGCbetai; soluble; guanylyloyclase betai; antiarteriosclerotic; vasotropic; hypotensive; gene therapy; arteriosclerosis; restenosis; ischemia; diagnosis; peripheral arterial occlusive disease; arterial hypertension.

Homo sapiens.

DE19837015-A1.

24-FEB-2000.

14-AUG-1998; 98DE-1037015

14-AUG-1998; 98DE-1037015.

(VASO-) VASOPHARM BIOTECH GMBH & S

Schmidt H, Zabel U, Poller W;

WPI; 2000-184044/17.

N-PSDB; AAZ88939

New human soluble guanylate cyclase alphal/betal and the nucleic acid

cell signalling;

insecticide;

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NO 1239

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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11-JUL-2000;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
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The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
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YKITERGEIDVKGKGTMGTYWLEEREN
                                                                 GIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQ
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AAY70475 standard; Protein; 690 ₿

AAY70475;

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cyclic nucleotide-associated protein-3 (CNAP-3).

AAY70474
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identified by PFAM analysis; CNAP-3 shares 89%
identity with human soluble guanylate cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNAP sequences may be used for prevention, treatment and diagnosis diseases associated with altered CNAP expression such as, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a human cyclic nucleotide associated protein-3 (CNAP-3), identified in Incyte clone 159278, that is isolated from ADENINBO1 CDNA library. It is expressed in nervous, reproductive, cardiovascular and developmental tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page
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6; Mismatches 219;
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                                                                                                                                                                                                                              This invention describes novel purified human soluble guanylate cyclase alphal/betal (hsGCalphal/betal). The products of the invention have antiarteriosclerotic, vasotropic and hypotensive activity. Nucleic acid sequences encoding the alphal and/or betal subunit are useful for somati gene therapy of arteriosclerosis and restenosis, ischemia (infarct), peripheral arterial occlusive disease and arterial hypertension.

Antibodies to hsGCalphal/betal can be used for diagnosis of aberrant hsGCalphal/betal expression in human tissues. This sequence represents the human soluble guanylylcyclase alphal subunit described in the method
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                                                                                                                  16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
                                                                                                                                                                  13-OCT-2000;
08-DEC-2000;
08-DEC-2000;
24-JAN-2001;
Detecting a prostate cancer-associated transcript in a cell in patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated
                                                                                                            04-MAY-2001;
                                                                                                                                                                                                                    12-OCT-2001;
                                                                                                                                                                                                                                      18-APR-2002.
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                                                                                                                                                                                                                                                                                              Prostate
                                                                                                                                                                                                                                                                                                                 Prostate cancer-associated
                                                                                                                                                                                                                                                                                                                                     15-AUG-2002
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                                                                                        (EOSB-)
                                                 2002-471335/50.
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                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TSRTETTGEKGKINVSEYTYRCL-----MSPENSDPQFHLEHRG
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                                                                      Mack
                                                                                        BIOTECHNOLOGY INC
                                                                                                         2000US-0687576.
2000US-0733288.
2000US-0733742.
2001US-263957P.
2001US-276791P.
2001US-276888P.
2001US-286214P.
2001US-286214P.
2001US-286214P.
2001US-286214P.
2001US-286589P.
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                                                                                                                                                                                                                    2001WO-US32045
                                                                     DH,
                                                                                                                                                                                                                                                                                              prostate tumour tissue;
                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                      Wilson
                                                                                                                                                                                                                                                                                                                protein #141.
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screening

genes

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RESULT 7
ABG61878
ID ABG6
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CC and another therapy, as a vaccine or in antisense applications.
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ABG61878
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                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                     TAICSQCS----PLQVITMLNALYTRFDQQCGELD---VYKVETIGDAYCVAGGLHKESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LILPGIIKAAAHVLYETEVEVSLM----PPCFHNDCSEFVNQPYLLYSVHMKSTKPS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIKESRKSLEREDFEKTIAEQAVAAGVPV-----EVIKESLGEEVFKICYEED-ENILG
                                                                                                                                                                             ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPG
                                                                                                                                                                                                                                TSRTETTGEKGKINVSEYTYRCL-----MSPENSDPQFHLEHRG
                                                                                                                                                                                                                                                                                                                                HHARSICHLALDMMEIAGOV-OVDGESVQITIGIHTGEVVTGVIGORMPRYCLFGNTVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKK-----SSRVMDLKGQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTEISCLRLKGQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLGSNVREFLQNLDAL-----HDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGLQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEIL-QMFGKMFFVFCQESGYDTILR 88
                                                                                                                                                                                                                                                                                  THAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVTQCGNAIYRVLPQLQ-PGNCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LSPSKPQSSLVIPTSLFCKTFPFHFMFDKDMTILQFGNGIRRLMNRRDFQGKPNF 320
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                                                  Protein;
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                                                  717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 789.5; DB 23; Pred. No. 1.5e-67;
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밁 Ş 밁 Ş 밁 QΥ 밁 δ 밁 δÃ 밁 δõ 밁 á 밁 Š 밁 Ş 밁

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concer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with comprises contacting a biological sample from the patient with comprises contacting a biological sample from the patient with comprises contacting only nucleotides (designated PC genes) that contact provides to a sequence that is at least 80% identical content of them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in contact cancer and are derived from the tissues of various content of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are cuseful for diagnosing or treating prostate cancer, as well as for contentifying modulators of prostate cancer or agents that inhibit contentifying modulators of prostate cancer or agents that inhibit content concer. The nucleic acid sequences are particularly useful concertance. ABG61800-ABG61944 represent prostate cancer-associated proteins.
                                                                                                                                                                                  Query Match
Best Local
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08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC. by determining if prostate cancer-associated grare expressed in a prostate tissue
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to methods of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; Page 363; 436pp; English.
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30-APR-2001;
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16-MAR-2001;
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DB; ABK92193.
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                                                                                                                                                                     182;
                                                                                                                                                                                   Similarity
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CSEFVNQPYLLYSVHMKSTKPS-----LSPSKPQSSLVIPTSLFCKTFPFHFMFDKD
                                                                                                       SILCLDRE-DDFLHVYYFFPRRTTSLILPGIIKAAAHVLYETEVEVSLM----PPCFHND
                                                                                                                                    SFRCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQ
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                                                                                                                                                                                                                                 717 AA;
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2001US-276791P.
2001US-276888P.
2001US-281922P.
2001US-286214P.
2001US-0847046.
2001US-288589P.
                                                                                                                                                                     Conservative
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2000US-0733742.
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                                                                       FLIEEKESKEEDFYEDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRD
                                                                                                                                                                                   22.6%;
36.9%;
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                                                                                                                                                                  Score 730.5;
Pred. No. 9.3e
80; Mismatches
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                                                                                                                                                                    Indels
                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate
                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
                                                                                                                                                                  Gaps
                                                                                                                                      178
                 286
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RESULT 8
ABB58042
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

(ABB57737-ABB72072).
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                                                                                                               Disclosure; SEQ ID NO 918; 21pp + Sequence Listing; English.
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                                                                                                                                                                                  WPI; 2001-656860/75
N-PSDB; ABL02145.
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11-JUL-2000;
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at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                   Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling (cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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DB; ABL14006.
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                            RPIAERMRKSEEHVCQSFEEVSVIFIEVM--NIYDSGSNNIQDAMQAVTTLNKV---FSA
                                                                                    NDLNPHGLSRELVMAGWQHCSKLEIMFEKEEQRSDELEKSLELADSWKRQGDELLYSMIP
                                                                                                                                             AATSKDEIDPATGQRRHSVGLRSILLKGQMFYIKDVDSLIFLCSPLIENLDELHGIGLYL
                                                                                                                                                                        ----EDEL---TGTE----ISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYL
                                                                                                                                                                                                     TVLFEFELIRTGHNRAAYDAALNFDFENFDEASSLNEAQAMALASAKEFSAENAKEEAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYGMLYESVQHYIQQEYGMETW---RKVCQIVDCKHQSFKTHQIYPDKLMPDFAAA----
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20000S-0614150.
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Pred. No. 2.9e-59;
3; Mismatches 264
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Matches 193; Conserv
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                                                                                                                                                                                                                                                                                                Disclosure;
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11-JUL-2000;
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                                                                                                                                                                                         (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                          invention relates to an isolated nucleic acid detection reagent
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                                    MYGMLYESVQHYVQEEYGVDIWRKVCHIIDC-KHNSFKTHQIYPDKLMPDIAEALSACTG
                                                          MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
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                                                                                   Conservative
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                                                                                 Score 685; DB 22;
Pred. No. 2.2e-57;
2; Mismatches 256;
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                                                                                                                                                                                                                                                                                      AAG00754 standard; Protein; 119
          N-PSDB;
                                        Dumas Milne Edwards
                                                                                  26-FEB-1999;
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          2000-500381/45.
DB; AAC00760.
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                                                                                                                                                                                                                                                                                                                                                                                   VVAGVVGQKVPRYCLFGDTVNTASRMESSSDPWKIQLSKYT-----GDKVRQVGYKVESR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELIRTGHNRAAYDAVLNMDFENYDEMDLNEAQTMALAKAQEFSESHPVDDDESAREDEID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLVRP-HIDISFHGI------LSHINTVFVLRSKE----GLLDVEKLECEDEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEEQVCQSFEEVSVIFLEVM--NVYDEGLNSIQGAMQTVNTLNKV---FSALDEEIISPF
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                                                                                                                                                                                          chromosome
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                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                        SEQ ID NO: 4835.
                                         Duclert
                                                                                                                                                                                        mapping.
                                                                                                                                                                                                   sequence tag; secreted protein;
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                                         Giordano
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to dealgn expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 4835; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                 ye number
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Matches 117; AAU11280 standard; 61 61 LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIYPGMRAPS Ľ 1 MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN LNAGETLQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIXXGMRAPS Conservative Protein; 1061 0; Score 599; DB 21; Pred. No. 3.3e-50; 0; Mismatches 2; B Indels 0, Gaps 119 119 60 0,

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Query Match Best Local

Local

Similarity

18.5%;

Length 119;

Sequence

119

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RESULT 12
AAU11280
Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; atrionatriuretic peptide receptor A; haplotyping; cytostatic; ge
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                         haplotype pair;
drug screening;
                                                                                                                                                                                                                           12-MAR-2002
                                                                                                                                                                                                                                          AAU11280
                                                                                                                                                                                                            atrionatriuretic peptide
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                       c peptide receptor A; haplotyping
single nucleotide polymorphism;
hypertension; hypotensive.
                                                                                                                                                                                                            receptor
                                                                                                                                                                                                            A (NPR1) protein
                                                                                                                                                                               gene
                                                                                                                                                                               therapy;
                                                                                                                                                                                       genotyping;
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Genotyping human natriuretic peptide receptor A/guanylate cyclase of an individual, involves determining identity of nucleotide pair specific polymorphic sites for two copies of the gene

pair

gene r at

Claim

27;

Fig

<u>ω</u>

96pp; English.

N-PSDB;

AAS16995

2002-066340/09.

Bentivegna SC,

Choi

JY,

Kliem

SE,

Nandabalan

14-APR-2000; 2000US-197330P. 16-APR-2001; 2001WO-US12300

(GENA-) GENAISSANCE PHARM INC

25-OCT-2001 WO200179231-A2

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1013 KIHLSSETKAVL----EEFGGFELELRGDVEMKGKGKVRTYWLLGERGSST 1059

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cc encoding the human natriuretic peptide receptor Ayguanylate cyclase A CC (atrionatriuretic peptide receptor A) guanylate cyclase A CC (atrionatriuretic peptide receptor A) or NPRI polypeptide. A method for CC haplotyping the NPRI gene in an individual comprises identifying the CC nuclectide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the NPRI haplotypes given in the specification or whether both copies are defined by a haplotype CC pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a CC trait and a haplotype or haplotype pair of the NPRI gene can be CC identified by comparing the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype CC frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. NPRI and its corresponding DNA are used for studying the expression and function of NPRI, for use in screening CC hypertension. The sequences are also useful for studying the effect of correspondences are also useful for studying the effect of correspondences are also useful for studying the effect of correspondences are also useful as on the binding caffinity of candidate drugs targeting NPRI. This sequence represents the cCC human NPRI polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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197; Conserv
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                                                                                                  MEIAGQVQV---DGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKG
                                                                                                                                                                                                                                   NLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIH----HARSICHLALDM
                                                                                                                                                                                                                                                                                                                            RKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAEST----PMQVV
                                                                                                                                                                                                                                                                                                                                                              KKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRRGLYLSDIPL-----HDATRDL------VLLGEQ--FREEYKLTQELEIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMRAPSFRCTDAEKGK--GLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRN 171
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                                                                                                                                                                                           TLLNDLYTCFDAVID----NFDVYKVETIGDAYMVVSGLP---VRNGRLHACEVARMALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CWAEDPQERPPFQQIRLTLRKFNRENSSNILDNLLSRMEQYANNLEELVEERTQAYLEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSFGIILQEIALRSGVFHVEGLDLSPKEIIERVTRGEQPPFRPSLALQSHLEELGLLMQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWMFRYSLTNDIVKGMLFLHNGAICS-------HGNLKSSNCVVDGRFVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EECDHTQFLIEEKESKEEDFYEDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RSAGSRLTLSGRGSNYGSLL----TTEGQFQV---FAKTAYYK--GNLVAVKRVNRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LALVGSLSLIGILIVSFFIYRKMQLEKELASELWRVRWEDVEP-----SSLERHL-----
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                                                             LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVVGLKMPRYCLFGDTVNTASRMESNGEAL
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Pred. No. 3.6e-37;
8; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QGHTVYAKKLWTAPELLRMASPPVRGSQAGDV
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NPR1 variant

polypeptide

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CC encoding the human natriuretic peptide receptor Ayguanylate cyclase A (atrionatriuretic peptide receptor Ayguanylate cyclase A (cc) (atrionatriuretic peptide receptor Ayguanylate cyclase A (cc) (atrionatriuretic peptide receptor A) or NPRI polypeptide. A method for Cc haplotyping the NPRI gene in an individual comprises identifying the Cc nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the NPRI haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype copairs can be assigned to specific genotypes. An association between a cc trait and a haplotype or haplotype pair of the NPRI gene can be cc identified by comparing the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype cr haplotype pair in a reference population, where a higher haplotype cr haplotype or haplotype pair. NPRI and its corresponding DNA are used cfor studying the expression and function of NPRI, for use in screening corrected or candidate drugs to treat diseases related to NPRI activity, such as higher thaplotype pair. The sequences are also useful for studying the effect of variation on the biological activity of NPRI as well as on the binding caffinity of candidate drugs targeting NPRI. This sequence represents a finity of candidate drugs targeting NPRI. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of an individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of the gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; atrionatriuretic peptide receptor A; haplotyping; cytostatic; ge haplotype pair; single nucleotide polymorphism; gene therapy; drug screening; hypertension; hypotensive.
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page -; 96pp;
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                         inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; hematopoletic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWMFRYSLTNDIVKGMLFLHNGAICS----
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tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiarthritic; haemostatic; antiarthreiosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
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27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ
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Human proteins and DNA encoding sequences useful for preventing treating or ameliorating a medical condition in a mammalian subg. arthritis or and subject

Claim 20; Page 246-247; 1963pp; English

haematopolesis regulatory activity; tissue growth activity; chamic conditions; chamic conditions activities; chamic conditions activities; activities; inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound the heat in these with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used to manipulate stem cells in culture to give rise to neuroepthelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may be used in cell cultures to give rise to neuroepthelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention. or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention me have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides Sequences ABB10981-ABB12330 represent 1350 novel polypeptides, an cell

Sequence 1075

Best Local Query Match al Similarity 197; Conserv Conservative 14.98; 27.78; , 88 Score 481.5; Pred. No. 3. Mismatches .7e-37; BB 22; Length 199; 1075; Gaps 31;

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RESULT 15
AAR38862
ID AAR38
XX AAR38
AC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
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  06-DEC-1990;
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                                                                                                      17-AUG-1993
                                                                                                                                                          US5237051-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                             enterotoxin; rat; small intestine;
receptor; bacterial enterotoxin;
ligand; antagonist.
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR38862-63 represent the guanylyl cyclases, GC-A and GC-B, which binds heat stable enterotoxin. These proteins are enterotoxin receptors which may be used as a therapeutic to contintestinal fluid permeation as well as abnormal conditions caused by bacterially released enterotoxin. The binding domain of the proteins, or antibodies to the proteins, can be used to eliminate diarrhoea. The proteins may be used to isolate ligands and to scree for antagonists of toxin binding.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified enterotoxin receptor protein - used to develop prods. for treating abnormal conditions caused by bacterially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVA-) UNIV VANDERBILT.
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                                                                                                                                                                                                                                                                                                                                   14.5%;
Similarity 43.4%;
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                              GKKEPMQVWFLSRKNTGT
                                                                                                                          VVSGLP----VRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVV
                                                                                                                                                                                        TIYFSDIVGFTALSAEST----PMQVVTLLNDLYTCFDAVID---NFDVYKVETIGDAYM
                                                                                                                                                                                                            TILFSGIVGFNAFCSKHASGEGAMKIVNILNDLYTRFDTLTDSRKNPFVYKVETVGDKYM
                                                                                                                                                                                                                                                    GKGKVRTYWLLGERGCST
                                                             GLKMPRYCLFGDTVNTASRMESNGEALKIHLSSETKAVL---EEFD-GFELELRGDVEMK
                                                                                        GQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLEHRGPVSMK
                                                                                                                                                      TVSGLPEPCIH----HARSICHLALDMMEIAGQVQV----DGESVQITIGIHTGEVVTGVI
                                                                                                                                                                                                                                                                                                                                                                                   1029 AA;
                                                                                                                                                                                                                                                                                                                     Conservative
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                              611
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Pred. No. 7.2e-36;
8; Mismatches 82;
                                                                                                                                                                                                                                                  :||:| : ||| :|| ||| :|:
-EEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSV
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Search completed: June 27, 2003, 13:03:03
Job time: 35.6287 secs

480 896 533 953 953

GenCore version: 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM prytein - protein search, using sw model

Run on: June 27, 2003, 13:03:07; Search time 17.4966 Seconds (without alignments) 3401.080 Million cell updates/sec

BLOSUM62 Gapop 10.0 , Gapext 0.5

Title:
Perfect score:
Sequence: US-09-762-767A-4
3231
1 MYGFYNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:*
pir2:*
pir3:*
pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

200 200 200 200 200 200 200 200 200 200	<u>.</u>	Result No.
987 987 960,55 955 955 955 957 957 957 957 957 957 9	3231	Score
28.7 29.5 29.5 29.6 28.3 28.3 28.3 28.3 28.3 28.3 28.3 28.3	100.0	Query Match
619 682 686 686 751 690 690 691 1099 717 683 583 583 583 1057 1057 1057 1057 1057 1057 1057 1057	619	Length
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159370	A89130	JC5581 T28130	B55915	JH0717	I59385	T42382	S45636	A55915	T24384	S33525	T28082	S55279	Т33167	
guanylate cyclase	protein F52E1.4 [1	guanylate cyclase hypothetical prote			guanylate cyclase	guanylate cyclase	natriuretic-peptid	guanylate cyclase	hypothetical prote	guanylate cyclase	hypothetical prote	guanylate cyclase	hypothetical prote	

ALIGNMENTS

RESULT 1 S23097 S23097 guanylate cyclase (EC 4.6.1.2), soluble, 70K chain - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000 C;Accession: S23097 R;Giulil, G.; Scholl, U.; Bulle, F.; Guellaen, G. FEBS Lett. 304, 83-88, 1992 A;Title: Molecular cloning of the cDNAs coding for the two subunits of soluble guanyl A;Reference number: S23097; MUID:92316204; PMID:1352257 A;Accession: S23097 A;Molecule type: mRNA A;Residues: 1-619 <giud 4731.3-4733<="" a;cross-references:="" a;map="" c;genetics:="" embl:x66533;="" gdb:141992;="" nid:g31685;="" omim:139397="" pid:g31686="" pidn:caa47144.1;="" positton:="" th=""></giud>
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C;Keywords: heterodimer; phosphorus-oxygen lyase F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>

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	Query Match Best Local : Matches 61
1 MY	tch al Sim 619;
GEVNHALE	ilarity Conserv
1 MYGFVNHALELLVIRNYGÞEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN 60	Query Match 100.0%; Score 3231; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e-215; Matches 619; Conservative 0; Mismatches 0;
HIII Wad	0, ,
EDIK	red.
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LVR	1; 15; 0;
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TYDLVA	619; 0;
ASKVLN	1; Length 619; 215; 0; Indels 0; Gaps 0
60	0;

Qy 361 EEYI 	Db 301 ISCI	Qy 301 ISCI	Db 241 PQL	Qy 241 PQL	Db 181 IEE	Qy 181 IEE	Db 121 RCTI	Qy. 121 RCTI	Db 61 LNAC	_	Qy 61 LNAC	1 61	61
EEYKLTQELEILIDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNV	ISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQFR	~	PQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTE		IEEKESKEEDFYEDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGNAIYRVL	- L.	RCTDAEKGKGLJLHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL		LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSF				
420	360	360	300	300	240	240	180	180	120	120		60	60

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RESULT 2
OYBO70

OYBO770

GUANNJIATE Cyclase (EC 4.6.1.2), soluble, beta-1 chain - bovine

N;Alternate names: guanylate cyclase, soluble, 70K chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-199
C;Accession: S01653; A38759
R;Koesling, D.; Herz, J.; Gausepohl, H.; Niroomand, F.; Hinsch, K.D.; Muel
FEBS Lett. 239, 29-34, 1988
A;Title: The primary structure of the 70 kDa subunit of bovine soluble gua
A;Reference number: S01653; MUID:89031214; PMID:2903071
A;Recession: S01653
A;Molecule type: mRNA
A;Residues: 1-619 <KOE>
A;Cross-references: EMBL:Y00770; NID:g407; PIDN:CAA68739.1; PID:g408
A;Cross-references: EMBL:Y00770; NID:g407; PIDN:CAA68739.1; PID:g408
A;Residues: 1-6;28-32;41-45;96-109;337-343;396-406;562-569 <KOE2>
A;Csuperfamily: soluble guanylate cyclase; guanylate cyclase catalytic doma
C;Keywords: CGMP blosynthesis: heterodimer; phosphorus-oxygen lyase
F;373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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                                                                                                                                                                                              RCTDADKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL
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                                                                                                                                                                                                                                                                                                                                                                  99.2%;
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Pred. No. 5.8e-214;
5; Mismatches 1;
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A;Title: Molecular cloning of a cDNA coding for 70 kilodalton A;Reference number: A31871; MUID:89087429; PMID:2905128
A;Molecular turn.
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A; Molecule: type: mRNA
A; Residues: 1-619 <NAK>
A; Residues: 1-619 <NAK>
A; Cross-references: GB:M22562; NID:g204273; PIDN:AAA41204.1; PID:g204274
A; Cross-references: GB:M22562; NID:g204273; pid:AAA41204.1; PID:g204274
C; Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic dom
C; Keywords: cGMP blosynthesis; heterodimer; phosphorus-oxygen lyase
F; 373-607/Domain: guanylate cyclase catalytic domain homology <GCC>
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9uanylate cyclase (EC 4.6.1.2), soluble, beta-1
N;Alternate names: guanylate cyclase, soluble, 7
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-19
C;Accession: A31871
C;Accession: A31871
R;Nakane, M,; Saheki, S; Kuno, T; Ishii, K; M
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Pred. No. 1e-212;
5; Mismatches 4;
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                                                                                                       GIVGFNAFCSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVSGL
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  PVPVESHAQRVANFALGMRISAKEVMNPVTGEPIQIRVGIHTGPVLAGVVGDKMPRYCLF
                       PEPCIHHARSICHLALDMMEIAGQVQ--VDGESVQITIGIHTGEVVTGVIGQRMPRYCLF
                                                                                                                                                                    SCOLEKKKEELRVLSNHLAIEKKKTETLLYAMLPEHVANQLKEGRKVAAGEFETCTILFS
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                                                                                  DVVTFTNIC---AACE-PIQIVNMLNSMYSKFDRLTSVHD---VYKVETIGDAYMVVGGV
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A;Accession: T23092
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-685 <WI
A;Cross references: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z19205
A; Accession: T19968
A; Status: preliminary; translated
A; Molecule type: DA:
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C; Superfamily: so
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KKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGFN---AFCSKHASGEGAM
                                      TSIPELLOYGLRLTAMPIHDPTRDLILLNQQRLSDVEMNLQLEANNEQLENMAKDLEVEK
                                                                                                                         MEFQRNANKRAAQAIEASENLYEDNNGALALSQSQHLKLKGQMMLMSSGGHIMYLCSPYV
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oluble guanylate cyclase; guanylate cyclase
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405/2; homology

212 TFCKAFPFHIIFDRDLYVTQCGNAIYRVLPQLQPGNCSLLSVFSLYRPHIDISFHGIL 269	1 MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN 60 : :::: : : : : : : : : : : : : : :	RESULT 6 T23721 T23721 T23721 Cypothetical protein M04G12.3 - Caenorhabditis elegans Cypothetics: Caenorhabditis elegans Cypothes: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000 Cypothes: 1998 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000 Cypothes: 1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000 Cypothes: 1998 #	
Qy 222 IFDRDLYVTQCGNAIYRVLPQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSK 281	1 MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN : ::::: :::	cal protein T04D3.4 - Caenorhabditis elegans : Caenorhabditis elegans 5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 on: T24458 , J. to the EMBL Data Library, October 1996 ce number: Z19893 op:eliminary; translated from GB/EMBL/DDBJ e type: DNA s: 1-751 <wild 1="" 149="" 1;="" 213="" 247="" 26="" 29.0%;="" 291="" 2;="" 332="" 35.0%;="" 369="" 3;="" 418="" 6.8e-57;<="" 751;="" 938;="" 95="" :="" atch="" cal="" catalytic="" cesp:t04d3.4="" cesp:t04d3.9="" clone="" cyclase="" cyclase;="" db="" domain="" dsp:t04d3.4="" efferences:="" embl:z81114;="" estal="" gspdb:gn00019;="" guanylate="" ition:="" length="" mily:="" no.="" pidn:cab03288.1;="" pred,="" s:="" score="" similarity="" soluble="" source:="" t04d3="" td=""><td>Qy 434CSKHASGEGAMKIVNILINDLYTREDILIDSKKNEFVYKVETVGDKYMTVSGLEEPCI 490 </td></wild>	Qy 434CSKHASGEGAMKIVNILINDLYTREDILIDSKKNEFVYKVETVGDKYMTVSGLEEPCI 490

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A;Gene: CESP:C06B3.8
A;Map position: 5
A;Introns: 1/3; 60/1; 192/3; 210/2; 270/2; 336/2; 415/2; 659
C;Superfamily: soluble guanylate cyclase; guanylate cyclase
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C;Speckes: Caenorhabditts elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T18984
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A; Residues: 1-699 <WIL>
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                                                                                           QELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSG
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                                                                                                                                              KGQMMLLASKKHIIYLCSPYVTSINELMQYGMRLTAMPLHDATRDLILLNQQRLSDVEVN
                                                                                                                                                                 KGQMIYLPEADSILFICSPSVMNLDDLTRRGLYLSDIPLHDATRDLYLLGEQFREEYKLT
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-CSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVS
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32.9%; Pred. No. 2.8e-55;
tive 132; Mismatches 234;
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(;Species: Homo sapiens (man)
(;C;Decies: Homo sapiens (man)
(;C)Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
(;Accession: S18325
R;Harteneck, C.; Wedel, B.; Koesling, D.; Malkewitz, J.; Boehme, E.; Schult:
FBBS Lett. 292, 217-222, 1991
A;Title: Molecular cloning and expression of a new alpha-subunit of soluble
A;Reference number: S18325; MUID:92070494; PMID:1683630
A;Accession: S18325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-732 <HARN

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S18325
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                 IY---PGMRAPSFRCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVAAASKVLNLNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLAT
                                                                                                                                                                                                                                                                                              LDDLTRRGLYLSDIPLHDATRDLYLLGEQFREEYKLTQELEILTDRLQLTLRALEDEKKK
                                                                                                                                                                                                                                                                                                                                                            LSTPFVIRTK----
                                                                                                                                                                                                                                                                                                                                                                                               INTVFVLRSKEGLLDVEKLECEDELTGTE--ISCLRLKGQMIYLPEADSILFLCSPSVMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVANEKLCSDVSNPGNCSCLTFLI--KECENTNIMKNLPQGTSQVPADLRISINTFCRAF
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                                                                                                                                            LNDLYTRFDTLTDSRKNPF--VYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIA
                                                                                                                                                                                       TVDLLYSIFPGDVAQQLWQGQQVQARKFDDVTMLFSDIVGFTAICAQCT----PMQVISM
                                                                                                                                                                                                                                                                      LDELMGRGLHLSDIPIHDATRDVILVGEQAKAQDGLKKRMDKLKATLERTHQALEEEKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                          PFHLMFDPSMSVLQLGEGLRKQL-----RCDTHKVLKFEDCFEIVSPKVNATFERVLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFHIIFDRDLVVTQCGNAIYRVLPQLQPGNCSLLSV-----FSLVRPHIDISFHGILSH
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                                                                                                    LNELYTRED-----HQCGFLDIYKVETIGDAYCVAAGLHRKSLCHAKPIALMALKMMELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 909.5; DB 2;
Pred. No. 6.1e-55;
1; Mismatches 175;
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homology

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guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - rat
N;Alternate names: guanylate cyclase, soluble, 77K chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31 Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A38297
R;Nakane, M.; Arai, K.; Saheki, S.; Kuno, T.; Buechler, W.; Murad, F.
J. Biol. Chem. 265, 16841-16845, 1990
A;Title: Molecular cloning and expression of cDNAs coding for soluble guanylate cyclase
A;Reference number: A38297; MUID:91009100; PMID:1698769
A;Accession: A38297
A;Molecule type: mRNA
A;Residues: 1-690 <ANAK>
A;Cross-references: GB:M57405; GB:M36075; NID:g204277; PIDN:AAA41206.1; PID:g204278
C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology
C;Reywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F;432-660/Domain: guanylate cyclase catalytic domain homology <GCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 214; Conserv
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                                                RGPVSMKGKKEPMQVWF
                                                                                                                LTSRTETTGEKGKINVSEYTYRCL---
                                                                                                                                                  DTHAVQIALMALKMMELSNEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVT
                                                                                                                                                                                                                                                 FNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPC
                                                                                                                                                                                                                                                                                GKLKATLEHAHQALEEEKKKTVDLLCSIFPSEVAQQLWQGQIVQAKKFNEVTMLFSDIVG
                                                                                                                                                                                                                                                                                                                                                     MIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRL
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                                                                               LANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSDIPGICHFLDAYQH
                                                                                                                                                                                                                  FTAICSQCS----PLQVITMLNALYTRFDQQCGELD---VYKVETIGDAYCVAGGLHRES
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A; Residues: 1-691 <KOE1>
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12
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R; Koesling, D.; Harteneck, C.; Humbert, P.; Bossernoii, FEBS Lett. 266, 128-132, 1990
A;Title: The primary structure of the larger subunit of A;Reference number: S10713; MUID:90306336; PMID:1973124
A;Accession: S10713
A;Accession: S10713
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A;Residues: 118-133;226-232;286-293;319-330;412-417;557-571;629-637 <KOE2>
C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic doma
C;Keywords: cGMP biosynthesis; heterodimer; phosphorus-oxygen lyase
F;434-662/Domain: guanylate cyclase catalytic domain homology <GCC>
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclase (EC 4.6.1.2), soluble, alpha-1 chain te names: guanylate cyclase, soluble, 77K chai
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                                                                                                                                                                                  VYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQ-VQVDGESVQITIGIHTGE
                                                                                                                                                                                                                                                                                   KRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPF
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   VFAGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREE
                                                          VVTGVIGORMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCL------MSPEN
                                                                                                                       VYKVETIGDAYCVAGGLHKESDTHAVQIALMALKMMELSHEVVSPHGEPIKMRIGLHSGS
                                                                                                                                                                                                                                                     GHAVQAKRFGNVTMLFSDIVGFTAICSQCS----PLQVITMLNALYTRFDRQCGELD---
                                                                                                                                                                                                                                                                                                                                                                             LRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKRKTVDLLCSIFPSEVARQLWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILRVLGSNVREFLONLDALHDHLATIYPGMRAPSFRCTDAEKGKG----
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Pred. No. 2.5e-45;
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hypothetical protein T07D1.1 - Caenorhabditis elegans ; Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C;Accession: T16822 R;Leimbac, D. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid :
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A; Reference number: Z18584
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                                                                                                                             HSGSVVAGVVGLSMPRYCLFGETVYVANKMEQNSSPMKILVSETTHNKI--
                                                                                                                                                          HTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDP-QF
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Pred. No. 8e-
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guanylate cyclase (EC 4.6.1.2) - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 26-Aug-1999
C;Accession: JH0810
R;Yoshikawa, S.; Miyamoto, I.; Aruga, J.; Furuichi, T.; Okano, H.; Mikoshiba, K.
J. Neurochem. 60, 1570-1573, 1993
A;Title: Isolation of a Drosophila gene encoding a head-specific guanylyl cyclas
A;Reference number: JH0810; MUID:93203896; PMID:8095978
A;Residues: JH0810
A;Rocession: JH0810
A;Rocelle type: mRNA
A;Residues: 1-683 <YOS>
A;Cross-references: GB:S57126; NID:9298674; PID:9298675
A;Experimental source: head
C;Genetics:
A;Gene: dgc 1
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A;Accession: $23098
A;Molecula type: mRNA
A;Residues: 1-717 <GIU>
A;Cross-references: EMBL:X66534; NID:g31683; PIDN:CAA47145.1;
C;Superfamily: soluble guanylate cyclase; guanylate cyclase cac;Keywords: heterodimer; phosphorus-oxygen lyase
F;430-658/Domain: guanylate cyclase catalytic domain homology
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S23098
R;Giuili, G.; Scholl, U.; Bulle, F.; Guellaen, G.
FEBS Lett 304, 83-88, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WQGQVVQAKKESNVTMLFSDIVGETAICSQCS----PLQVITMLNALYTREDQQCGELD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSEFVNQPYLLYSVHMKSTKPS-----LSPSKPQSSLVIPTSLFCKTFPFHFMFDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILCLDKE-DDFLHVYYFFPKRTTSLILPGIIKAAAHVLYETEVEVSLM----PPCFHND
                                                                                                                                                                                                                                                                                                                                                                                             ENSDPQFHLEHRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKK------SSRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEKLECEDELTGTEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTILQFGNGIRRLMNRRDFQGKPNFEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNS
                                                                                                                                                                                                                                                                                                                                                          EELPPNFPSEIPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FLIEEKESKEEDFYEDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRD
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Pred. No. 1.5e-42;
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protein C54E4.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88642
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9951916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: special sequence of the consortium and compared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: F88642
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:chr_IV; PIDN:AAB92031.1; PID:g2702405; GSPDB:GN00022; CESP:C54E4
A;Note: Similar to guanylate cyclase
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F88642
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C;Superfamily: soluble guanylate cyclase; guanylate cyclase catalytic domain homology C;Reywords: cGMP blosynthesis; phosphorus-oxygen lyase F;417-641/Domain: guanylate cyclase catalytic domain homology <GCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 TEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKESKEEDFYEDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGNAIYRVL-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGRKMPRYCLFGHSVTIANKFESGSEALKINVSPTTKDWLTKHEGF--EFELQPRDP-SF 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVTILFSGIVGENAFCSKHASGEGAMKIVNLLNDLYTRFDTLITDSRKNPF--VYKVETVG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FREEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYD 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LEIKGQMVHCPESNSLLFIGSPFLDGLDGLTCNGLFISDIPLHDATREVILVGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YMADFGCQATTYFDFKRPKGLTMKFRDIVRRTYTPFLIGLNNPPGAVDFPAIG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTSVSKTIPETVQRSNSSNASDLQMNSSSFCKMFPWHFIMNEQLELVQLGRGFSKLYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERPVIAWLLLGSLKALTRMLYKVDVNIKI--EPVERCPAVSLPLLAGQGQLPDHAD---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEEC-------DHTQFLIE 182
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No. 2.6e-41;
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A;Gene: C54E4.3
A;Map position: 4
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Query Ma	Query Match 21.7%; Score 701.5; DB 2; Length 583; Best Local Similarity .29.6%; Pred. No. 1.16-40;	
Matches	172; Conservative 139; Mismatches 207; Indels 63; Gaps 17	7
Qy	26 KKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEILQMFGKMFFVFCQESGYDT 85	
B	20 RRKAGYQEDIKEDIQCYYDDTETMRIFRVAATVLGLSVDDMWEMYGEFLITHACETGWQK 79	
Qy	86 ILRVIGSNVREFIGNIDALHDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGL 142	N
рь	80 MIFCMANNIQEFIDNINSMHYFIDQIA-FKSEMKGPTFQCEPFGE-SGIKIHYFSFRQGI 137	7
Qy	143 QDIVIGIIKTVAQQIHGTEIDMKV-IQQRNEECDHTQFLIEEKESKEEDFY 19:	N
Db	138 FPIVKGLVRKTARTLFEMDVKVCMLERNQERKKSGMVEHVIFSVEPDDNHRKGKRLFH 195	5
Qy	193 EDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGNAIYRVLP 241	\vdash
Db	196KFRNTKTTENAPS-FTLSSTILVGLRDFKNIFPYHVCFNKQMIIEHIGIYLLREYG 250	0
Оy	242 QLQPGNCSLLSVFSLVRP-HIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTE 300	0
DЪ	251 LENKKTLKVSDLMQLVQPSDIQLTYKNVLSYLNTLFIFQLKHHSKRNEVQEGSSEAF 307	7
Qy	301 ISCLRLKGOMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEOFR 36	0
DЪ	308 QQPLVLKGEMMPINDGNSIIFICSPHVTTVRDILNLKLXISDMPMHDATRDLVMLNQSRI 367	7
Qy	361 EEYKLTQELEILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPA 414	4
Db	368 CQNELNKKLEETMKKMKMTEELEVKKSQTDRLLFEFVPPVIAEALRAAKTVPALMQKRI 427	7
Qy	415KRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKN 460	σ
DЪ	428 SIDESEEFSDCSVIFTDIPDFFTISVNCSPTEIITVVTDLFHRFDRIIEKHKG 480	0
Qy	467 PEVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQVQVDGESVQITIGIH 524	4
Db	481YKVLSLMDSYLIVGGVPNANQYHCEDSLNLALGLLFEAKQVVVPKLERSVRLRIGVH 537	7
Qy	525 TGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVS 565	
망	538 CGPVVAGIVSQQKPRFCVLGNTVNVTKSICSHSSPGKVLVS 578	

Search completed: June 27, 2003, 13:05:25 Job time: 19.4966 secs

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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 11.0695 Seconds (without alignments) 2585.358 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-762-767A-2 3593 1 MFCTKLKDLKITGECPFSLL.....QKKDVEDGNANFLGKASGID 690

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	33	3 2	3 6	29	28	27	26	25	24	23	22	. 21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	_	No.	Result
	399.5	408.5	414.5	427	428.5	430	434	438	438	440	442	445	448	450	452	454.5	456.5	457.5	460	460	460	708	774.5	•	793.5	795	976.5	1635	1651	3107.5	3232	3593	Score	
	11.1	11.4		11.9			12.1	12.2	12.2	12.2	12.3	12.4	12.5	12.5	12.6	12.6	12.7					19.7		•	•	•	•	45.5		٥.	90.0	100.0	Match 1	Operv
	1076	1073	1073	1125	1050	1110	1103	1110	1108	1103	1108	1109	1108	1108	433	1057	1061	1057	1047	1047	1047	617	682	619	619	619	683	732	730	691	690	690	Length D	
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	HSER_CAVPO	HSER_HUMAN	HSER_PIG	CYGS_STRPU	ANPB_ANGJA	CYGX_RAT	CYGD_HUMAN	CYGD_BOVIN	CYGF_RAT	CYGF_BOVIN	CYGF_HUMAN	CYGD_CANFA	CYGE_RAT	CYGE_MOUSE	KSGC_RAT	ANPA_MOUSE	ANPA_HUMAN	ANPA_RAT	ANPB_RAT .	ANPB_HUMAN	ANPB_BOVIN	CYG2_HUMAN	CYG2_RAT	CYG1_HUMAN	CYG1_BOVIN	CYG1_RAT	CYGH_DROME	CYG4_HUMAN		CYG3_BOVIN		CYG3_HUMAN	ID	
-	P70106 cavia porce					rattu			ratt									-		P20594 homo sapien				homo					rat		rattu	ā	Description	

EMBL; X66534; CAA47145.1; -. EMBL; U58855; AAB94794.1; -.

5	44	43	42	41	40	39	38	37	36	ယ	34
287.5	290.5	302	303	303.5	310.5	316	319	319.5	322	322.5	389
8.0	8.1	8.4	8.4	8.4	8.6	8.8	8.9	8.9	9.0	9.0	10.8
1249	2248	1134	1144	1144	1078	1080	1090	1099	1064	887	1137
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CYA8_MOUSE	CYA1_DROME	CYA1_BOVIN	CYA3_RAT	CYA3_HUMAN	CYA7_BOVIN	CYA7_HUMAN	CYA2_RAT	CYA7_MOUSE	CYA4_RAT	CYA2_HUMAN	CYG1_CAEEL
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P97490	P32870 drosophila	19754	21932	60266	29450	51828	26769	51829	26770	08462)9435

ALIGNMENTS

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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001054; G_cyclase. Pfam; PF00211; guanylate_cyc; 1 SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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MIM; 139396; -.
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323098; S23098.
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                                                                     SRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQAR
QQGTNSKPCFQKKDVEDGNANFLGKASGID
                                         VTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPGICHFLDAY
                                                                                                                                                                                                                                                 FGNGIRRLMNRRDFQGKPNFEEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKKS
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                                                                                                               TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHK
                                                                                                                          TMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLHK
                                                                                                                                                                                                                                                                                                                                                              QAVAAGVPVEVIKESLGEEVFKICYEEDENILGVVGGTLKDFLNSFSTLLKQSSHCQEAG
                               VTLANKFESCSVPRKINVSPTTYRLLKDCPGEVFTPRSREELPPNFPSEIPGICHFLDAY
                                                                                                                                                       AQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNV
                                                                                                                                                                AQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNV
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GDAYCVA -> AMPIVWL (IN REF. 1).

GNANFLGKASGID -> ASQFFRQSIRNRLATYIPIYKSLG

FDSLKWCRASESTLGIYUG (IN REF. 1).

DA1E14A5E11451CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE CYCLASE.
AAGV -> QOS (IN REF. 1).
VIKESLGEFURKICYEBEBNILGVVGGTLKDFLNSFSTLLK
OSSHCQEAGKRGR -> LSKNLLVKRFLKYVTRKMKTSLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3593; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEAPLKIFKQLQYPSETEQPLPRSRKKGQ
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59 120

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661 QQGTNSKPCFQKKDVEDGNANFLGKASGID 690
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STRAIN-Sprague-Dawley: TISSUE-Striatum;

X MEDLINE-97151525; PubMed-8997507;

X MEDLINE-97151525; PubMed-8997507;

A Smigrodzki R.M., Levitt P.;

The alpha 1 subunit of soluble guanylyl cyclase is expressed prenatally in the rat brain.";

I prenatally in the rat brain.";

I prenatally in the rat brain.";

C --- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C --- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF LEXYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF MAGNESIUN OR MANGANESE IONS.

C --- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C --- SUBCELLULAR LOCATION: Cytoplasmic.

C --- SUBCELLULAR LOCATION: Cytoplasmic.

C --- SUBCELLAREOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLEONS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYG3_RAT
P19686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the long as lon
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC
(Soluble guanylate cyclase large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakane M., Arai K., Saheki S., Kuno T., Bue "Molecular cloning and expression of cDNAs guanylate cyclase from rat lung."; J. Biol. Chem. 265:16841-16845(1990).
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00452; GUANYLATE_CYCLASES 1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
Lyase; cGMP synthesis; Multigene family.
DOMAIN 480 607 GUANYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M57405; AAA41206.1;
EMBL; U60835; AAB17953.1;
PIR; A38297; OYRTA1.
HSSP; P19687; IAWN.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUCY1A1 OR GUC1A1.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001054; G_cyclase.
                                                                                                                                                              al Similarity
616; Conserv
                                          MFCTKLKDLKITGECPFSLLAPGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESLP
MFCRKFKDLKITGECPFSLLAPGQVPTEPIEEVAGVSESCQATLPTCQEFAE-NAEGSHP
                                                                                                                                                                                                                                                                                                                                 690 AA;
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                                                                                                                                                                                                                                                                                                                                 77566 MW;
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                                                                                                                                                                                                Score 3232; DB 1;
Pred. No. 4.3e-218;
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                                                                                                                                                                                                                                                                                                                                     CRC64;
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T 01-FEB-1991 (Rel. 17, Last sequence update)
T 16-CCT-2001 (Rel. 40, Last annotation update)
E Guanylate cyclase soluble, alpha-1 chain (EC 4.6
S (Soluble guanylate cyclase large subunit).
S GUCYIA1 OR GUCIA1.
S Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
enzyme.";
FEBS Lett. 266:128-132(
[2]
3D-STRUCTURE MODELING O
MEDLINE-98054247; PubMe
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P19687;
01-FEB-1991
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                                                               Koesling
Schultz G
"The prim
                                                 cyclase f
enzyme.";
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G., Boehme
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                                    266:128-132(1990)
                                                      structure of bovine lung.
                                                                                 Harteneck C.,
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        PubMed=9391039;
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                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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       VTMLFSDIVGFTAICSQCSPLQVITMLNALYTRFDQQCGELDVYKVETIGDAYCVAGGLH
                                                      RAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSN
                                                                                           SSRVMDLKGQMIYIVESSAILFLGSPCYDRLEDFTGRGLYLSDIPIHNALRDVYLIGEQA
                                                                                                                                                       DQAIAAGVPVEIIKESLGEELFKICYEEDEYILGVVGGTLKDFLNSFSTLLKQSSHCQEA
                                                                                                                                                                                                                                                                     PRRKTSRSRYYLHTLAESICKLIFPEFERLNLALQRTLAKHKIKENRKSLEREDFEKIVV
                                                                                                                                                                                                                                                                              PQRKTSRSRVYLHTLAESICKLIFPEFERLNVALQRTLAKHKIKESRKSLEREDFEKTIA 119
                                                                                                                                                                                                                                                                                                         MFCAKLKDLQITGDCPFSLLAPGQVPREPLGEATGSGPASTPGQPGVCPGVPDKNPPGRL
                                                                                SSRVMDLKGQMIYMVESSSILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQA
                                             RAQDGLKKRLGKLKATLEQAHQALEEEKRKTVDLLCSIFPSEVARQLWQGHAVQAKRFGN
                                                                                                                                                                                                                                                                                                                                              Conservative
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86.5%;

41;

Score 3107.5; DB 1; Pred. No. 2.1e-209; 1; Mismatches 54;

Indels Length

1;

Gaps

60 59

179 120

240 239 180

420

360 359 300 691;

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SO THE REAL PROPERTY OF THE RE
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                                                                                                                                                                                                                                                                                                                                                                                X54014; CAA37960.1;
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                                                                             Query Match
Best Local Sir
Matches 355;
                                                                                                                                                 InterPro; IPRO01054; G_cyclase.

Pfam; PP60211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.

Lyase; CGMP synthesis; Multigene family.

DOMAIN 519 646 GUANYLATE CYCLASE.

DOMAIN 50 72 ALA-RICH.

DOMAIN 50 72 POLY-ALA.

SEQUENCE 730 AA; 81786 MW; B8D790BFF81FB8F9 CI
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or send a
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STRAIN-Wistar Kyoto; TISSUE-Aorta;
MEDLINE-20571097; PubMed-11121588;
                                                                                                                                                                                                                                                                                                                                       EMBL; AF109963; AAD42949.2; HSSP; P19687; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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an email to license@isb-sib.ch).
                                                                                                Similarity
         GECPLSKLCWNGSRSPPG--
                                         GECPFSLLA-----PGQVPNESSEEAAGSSESCKATVPICQDIPEKNIQESL-----
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soluble, alpha-2 chain (EC
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Pred. No. 1.1e
06; Mismatches
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                                                                                                                                                     B8D790BFF81FB8F9 CRC64;
         --PPGSRAAAMAATP---
                                                                                            1651; DB 1;
No. 1.1e-107;
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D7 01-FEB
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DE GUANY1
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-2 chain (EC GUCYIA2 OR GUCIA2 OR GUCSA2.
                                               guanylyl
enzyme."
                                                                                                          SEQUENCE FROM N.A. MEDLINE-92070494; Harteneck C., Wede
                                                                                                                                                                                     NCBI_TaxID=9606;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                       CYG4_HUMAN
                                                                                              Schultz
                                                                       Molecular cloning
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                                                                                                               Wedel
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                                                                                                          PubMed=1683630;
el B., Koesling
                                                      and expression of 
Interchangeability
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Primates;
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                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                        of
                                                                                                           Malkewitz J.,
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f the alpha-subunit
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                                                     alpha-subunit of soluble alpha-subunits of the
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                                                                                                             Boehme
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Best Local Similarity
Matches 355; Conserv
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PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.
Lyase; CGMP synthesis; Multigene family; Alternative splicing.
DOMAIN 521 648 GUANYLATE CYCLASE.
DOMAIN 51 76 ALA-RICH.
DOMAIN 51 76 ALA-RICH.
DOMAIN 51 58 POLY-ALA.
TARSPLIC 612 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaborabetween the Swiss Institute of Bioinformatics and the EMBL outstat. the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X63282; CAA44921.1; -.
EMBL; Z50053; CAA90393.1; -.
PIR; S18325; S18325
HSSP; P19687; 1AWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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"A variant of the alpha 2 subunit of soluble guanylyl cyclase
contains an insert homologous to a region within adenylyl cyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM ALPHA 2-I). MEDLINE-95403342; PubMed-7673142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS EXPRESSED ONLY IN LIVER, COLON AND ENDOTHELIUM.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUARYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
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GFDALLE---HIRTSFGKQATLESPSFLCKELPEGTLMLHYFHPHHIVGFAMLGMIKAAG
                                           SFSTLLKQSSHCQEA-GKRGRLEDASILCLDKEDDFLHVYYFFPKRTTSLILPGIIKAAA
                                                                                                                RRRVNLDSLGESISRLTAPSPQTIQQTLKRTLQYYEHQVIGYRDAEKNFHNISNRCSYAD
                                                                                                                                                                                                                                                                         GECPLSRICWNGSRSPPG--PLEPSPAAAAAA----AAPAPTPAASAAAAATAGARRVQR 81
                                                                                        HSNKEEIEDVSGILQCTANILGLKFEEIQKRFGEEFFNICFHENERVLRAVGGTLQDFFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ALA.

Q -> QEBELLESEPVSIQLVPDQHQSETDLGTEK
(IN ISOFORM ALPHA 2-1).

79465A7D3FE52DB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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AS A NEGATIVE
S NON-FUNCTIONAL
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Q07093;
Q1-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Head-specific guanylate cyclase (EC 4.6.1.2).
GYC-ALPHA-99B OR GYC-ALPHA-63A OR GYC OR DGC1.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                             J. Neurochem. 60:1570-1573(1993).

-!- FUNCTION: MAY HAVE A ROLE IN PHOTOTRANSDUCTION. A SECOND MAY BE REQUIRED FOR ENZYME ACTIVITY.

-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

-!- SUBUNIT: DIMER (PROBABLE).
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Canton-S; TISSUE-Head;
MEDLINE-93203896; PubMed-8095978;
                                                                                                                                                                                                                                                               cyclase."
                                                                                                                                                                                                                                                                                              Yoshikawa S., Miyamoto I., Aruga J.,
Mikoshiba K.;
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                              'Isolation of a Drosophila gene
                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (Potential).
TISSUE SPECIFICITY: HEAD, WHERE IT IS PREFERENTIALLY EXPRESSED IN
THE CNS AND THE RETINA. NOT FOUND IN BODIES.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                     FAMILY.
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Best Local Similarity
Matches 244; Conserv
                                       CYG1_RAT
P20595;
01-FEB-1991
01-FEB-1991
16-OCT-2001
O1-FEB-1991 (Rel: 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-1 chain (EC 4
(Soluble guanylate cyclase small subunit).
GUCY1B1 OR GUCY1B3 OR GUCLB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flybase; FBgn0013972; Gyc-alpha-99B.
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
SMART; SM00044; CYCc; 2.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; FALSE_NEG.
PROSITE; PS00155; GUANYLATE_CYCLASES_2; 1.
Lyase; cGMP synthesis; Multigene family; Vision.
DOMAIN
465
591
GUANYLATE_CYCLASE.
SEQUENCE 683 AA; 75906 MW; 12D67C4B79A07C8D CRC64;
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HSSP;
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JH0810; JH0810.
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                                                                                                                                                                        ALKINVSPITKDWLTKHEGFEFELQPRDPSFLPKEFPN--PGGTETCYFLESFR
                                                                                                                                                                                           PRKINVSPTTYRLLKDCPGFVF--TPRSREELPPNFPSEIPG---ICHFLDAYQ
                                                                                                                                                                                                                                                          ALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTLANKFESCSV
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Pred. No. 1.3
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Best Local Similarity
Matches 210; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M22562; AAA41204.1; PIR; A31871; OYRTB1.
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PROSITE; PS50125; GUANYLATE_CYCLASES.
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InterPro; IPR001054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: LUNG AND BRAIN.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
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NALRDVVLIGEQARAQDGLKKRLGKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQL
                                                                                                                                  VKK---
                                                                                                                                                                           VVTQCGNAIYRVLPQLQ-PGKCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLD
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                                                                                    VEKLECEDELTGAEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLH
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619 AA;
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Rodentia;
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                                                                                                           SSRVMDLKGQMIYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ore 795; DB 1;
ed. No. 5.2e-48;
Mismatches 225;
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CYGL_DAYN
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DE GUANY
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OC EULARY
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T "Catalytic mechanism of the adenylyl and guanylyl cyclases: mode mutational analysis.";

Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

C -!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C -!- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE MAGNESIUM OR MANGANESE IONS.

C -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -!- SUBCELLAR LOCATION: Cytoplasmic.

C -!- MISCELLAR DECLIFICITY: LUNG AND BRAIN.

C -!- MISCELLARDOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SO FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

C -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-1 chain (EC 4
(Soluble guanylate cyclase small subunit).
GUCYIBI OR GUCYIB3 OR GUCIB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The primary structure of guanylate cyclase."; FEBS Lett. 239:29-34(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koesling D., Herz J., Gausepohl H.,
Muelsch A., Boehme E., Schultz G.,
"The primary structure of the 70 kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
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MEDLINE=89031214;
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P16068;
                                                                                                                                                       or send an
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Liu Y., Ruoho A.E., Rao V.D., Hur
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                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced th een the Swiss Institute of Bioinformatics and t
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                                                    1AWN;
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                                                                                                                                                  requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                    non-profit institutions as long and this statement is not removed.
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  guanylate_cyc;
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RP SEQUEN
RC TISSUE
RT MOLEC
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Best Local S
Matches 208
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(Q02153;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (GCS-beta-1)
(Soluble guanylate cyclase small subunit) (GCS-beta-3).

GUCY1B1 OR GUCY1B3 OR GUC1B3 OR GUCSB3.
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 MEDLINE-92316204; pubMed-1352257;
Giuili G., Scholl U., Bulle F., Guellaeen G.
"Molecular cloning of the cDNAs coding for t
soluble guanylyl cyclase from human brain.";
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                                                         TISSUE-Brain;
                                                                    SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID=9606;
                                                                                                             Mammalia;
                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                      Homo sapiens (Human)
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Pred. No. 6.0
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splicing.";
FEBS Lett. 290:157-158(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
LYase; CGMP synthesis; Alternative splicing
DOMAIN 421 554 GUANYLATE CYCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the surpression of the su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92008652; PubMed-1680753; Chhajilani V., Fraendberg P.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
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HSSP; P16068; 1AWN.
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Pfam; PF00211; guanylate_cyc; 1.
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HSGC-1 (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLAS FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
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EEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKK--
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G-1997) to the EMBL/GenBank/DDBJ databases
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MISSING (IN ISOFORM HSGC-2).
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Pred. No. 1.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-2 chain (EC 4.6.1.2)
GUCYIB2.
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           InterPro; IPR001054; G_cyclase.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR0011230; Prenyl_site.
IPfam; PF00211; guanylate_cyc; 1.
SMARR; SM00044; CYCc; 1.
SMARR; SM000452; GGANYLATE_CYCLASES_1;
PROSITE; PS00452; GUANYLATE_CYCLASES_2;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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or send a
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 29:10872-10878(1990).
-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic
-!- ENZYME REGULATION: ACTIVATED BY NITRIC
                                                                                                        EMBL; M57507; AAA41207.1;
PIR; A36228; OYRTB2.
HSSP; P19687; IAWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91105012; PubMed-1980215;
Yuen P.S.T., Potter L.R., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
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kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: KIDNEY AND LIVER.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
                                                                                                                                                                                                                                                                                                                                                                                             MAGNESIUM OR MANGANESE IONS.
SUBUNIT: HETERODIMER OF AN ALPHA AND
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Best Local
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075343; Q9NZ64;
15-JUL-1999 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                             Behrends S., Vehse K.;
Behrends S., Vehse K.;
The beta(2) subunit of soluble guanylyl cyclase contains human-specific frameshift and is expressed in gastric carrenates at an expression of the contains human-specific frameshift and is expressed in gastric carrenates. Res. Commun. 271:64-69(2000).
SEQUENCE OF 95-257
TISSUE-Heart;
MEDLINE-99107820;
                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    GUCY1B2
                                                                                                                                                            Guanylate cyclase
                                                                                                              NCBI_TaxID=9606;
                                                                          MEDLINE=20241821; PubMed=10777682;
                                                                                  FISSUE=Kidney;
                                                                                           SEQUENCE FROM N.A., AND REVISION
                                                                                                                                          Homo sapiens (Human)
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Genomics 55:126-127(1999).
I- CARALYTIC ACTIVITY: GTP = 3',5'-cyclic - ENZYME REGULATION ACTIVATED BY NITRIC MAGNESIUM OR MANGANESE IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001054; G_cyclase.
Pfam; Pr00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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EMBL; AF218383; AAF66105.1;
HSSP; P19687; 1AWN.
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MIM; 603695; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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SUBCELLGUAR LOCATION: CYCOPLASMIC.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                             LKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGFT
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the Euro
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_BOVIN
                                                                         EMBL;
EMBL;
HSSP;
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"Detection of expression of a membrane form of
type of GC-B in cattle retina (letter).";
Bioorg. Khim. 19:682-685(1993),
-I- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC
   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide
                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95147885; PubMed-7845391;
Fenrick R., Babinski K., McNicoll N.,
                                    InterPro;
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93371497; PubMed-8103329;
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NCBI_TaxID=9913;
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                                                     InterPro;
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CATALTYTC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphat.
SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECE
WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND OF
WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP ICIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CANDOMAIN OF PROTEIN KINASES.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLY.
                                                                                                                                                                                                             ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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                                                                  L26359; AAC41619.1;
X66865; CAA47334.1;
Q02846; IAWL.
                                                                                                                                              an
                                                                                                                                          non-profit institutions as long
and this statement is not removed.
requires a license agreement (See
an email to license@isb-sib.ch).
                IPR001828;
IPR000719;
IPR001054;
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; ANF_receptor.
; Euk_pkinase.
; G_cyclase.
; Ntpep_receptorn.
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Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF01094; ANF receptor; 1.

PRINTS; PR00255; NATPEPTIDER.

PRODOm; PD000001; Euk_pkinase; 1.

SMART; SM00044; CYCc; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

R PROSITE; PS00458; GUANYLATE_CYCLASES_1; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
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Best Local
                                                                                                                01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor B precursor
(Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial
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P20594; Q9UQ50; O60871;
O1-FEB-1991 (Rel. 17, Cr.
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                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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439
448
                                   Chordata;
Primates;
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ATRIAL NATRIURETIC F
EXTRACELULAR (POTEN
POTENTIAL.
CYTOPLASMIC (POTENT)
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (PROBABLE)
                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ţ
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1A3814D02F22D64F
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; Phosphorylation;
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Length 1047;

CRC64;

(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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) (POTENTIAL).
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Indels

42;

LKATLEQA Gaps

995 612 558

499 819 439

879

PEPTIDE

RECEPTOR

Lyase;

(ANP-B) (ANPRB) (GC-B) natriuretic peptide

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C -I- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANT. SEEMS TO BE STIMULATED MORE CEFECTIVELY BY BRAIN NATRIURETIC PEPTIDE (BNP) THAN BY AND.

C -I- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C -I- SUBCELLULAR LOCATION: Type I membrane protein.

C -I- SUBCELLULAR LOCATION: Type I membrane protein.

C -I- ALITERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM/NER-BI; ARE PRODUCED BY ALITERNATIVE SPLICING.

C -I- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS; TWO WITH GUANYLATE CYCLASE ACTIVITY (AND-A AND AND-B) AND ONE (AND-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

C -I- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirsch J.R., Herter P., Welkruhoffer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Differential activation by atrial and brain natriuretic peptides of two different receptor guanylate cyclases.";
Nature 341:68-72(1989).
   EMB1, 1809 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           natriuretic peptides. Molecu proximal tubule cells."; Submitted (APR-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Izumi Y., Kanmatsuse K., Ozawa Y.;
"Structure of the type B human natriuretic peptide
association of a novel microsatellite polymorphism
hypertension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99182382; PubMed-10082481; Rehemudula D., Nakayama T., Soma M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "cGMP-dependent and independent inhibition natriuretic peptides. Molecular and function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
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TISSUE-Brai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
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AB005631,
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AB005633,
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AB005626;
AB005627;
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InterPro; IPR000719; E
InterPro; IPR001054; C
InterPro; IPR001170; N
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SEQUENCE
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smart; SM00044; CYCC; 1.
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50111; PROTEIN_KINASE_DOM; 1.
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EMBL;
PIR; §
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MIM; 108961; -.
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ALKIHVSSTTKDALDELGCFQLELRGDVEM
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                    PRKINVSPTTYRLLKDCPGFVFTPRSREEL
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S05514.
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Euk_pkinase.
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; Glycoprotein; Phosphorylation; Lyase;
Alternative splicing; Polymorphism.
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Pred. No. 2.6e-24;
Pred. No. 2.6e-24;
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TKDALDELGCFQLELRGDVEMKGKGKMTTYWLLGERKGFBG
LL -> KADSHSSPELHLSQTLPTCFFSKGQSVLGLLA
(IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTI
PROTEIN KINASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                              Q -> E (IN DBSNP:5816).
/FTId=VAR_011968.
T -> S (IN REF. 2).
W; 817FB74D6B31F7EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUANYLATE CYCLASE
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ATRIAL NATRIURETIC
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INTERCHAIN (PROBABLE)
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                         Gaps
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ANPB_RAT
                                                                                                                                                                                                                                                     Pfam; PF00069; pkinase; 1.

Pfam; PF00069; pkinase; 1.

Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF00251; NATF_TECEPTOT; 1.

PRINTS; PR00255; NATF_PETIDER.

PTODOM; PD000001; Euk_pkinase; 1.

SMART; SM00044; CYCG; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00458; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMULATED MORE EFFECTIVELY BY BRAIN NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMULATED MORE EFFECTIVELY BY BRAIN NATRIURETIC PEPTIDE (BNP) THAN BY ANP. I. CARTON: TYPE J. S. S. C. CYCLIC GMP + diphosphate.

1. SUBCELLULAR LOCATION: TYPE I membrane protein.

1. MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

1. SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.

1. SIMILARITY: BELONGS TO ADENVILLY TOWARD REGION OF CATALYTIC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M26896;
PIR; A33300;
     DOMAIN
DOMAIN
DISULFID
                                                                               TRANSMEM DOMAIN.
                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001828; ANF_receptor.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_receptorN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The primary structure demonstrates diversity Cell 58:1155-1162(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                           Receptor; Trans
cGMP synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide
                                                                                                                                      DOMAIN
                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B-type receptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (See http://www.isb-sib
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                   Transmembrane;
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S., Bellet R.A.,
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                                                                                                                                                                                                                                   lycoprotein;
POTENTIAL.

ATRIAL NATRIURETIC PEPTIDE EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

PROTEIN KINASE-LIKE.

GRANYLATE CYCLASE.

BY SIMILARITY.
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in this
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Best I
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                                                             MEDITINE-91056089; PubMed-1978722; Yamaguchi M., Rutledge L.J., Garbers I Yamaguchi maray structure of the rat guar natriuretic peptide receptor gene."; J. Biol. Chem. 265:20414-20420(1990).
                                                                                                                                                                                                                                                                                                                         ANPA_RAT
P18910;
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DISULFID
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
SEQUENCE
                                                                                                                                        Goeddel D.V., Schurz ...
"A membrane form of guanylate
"A membrane form of guanylate
                   Duda T., Goracz
Site-directed
                                                                                                                                 peptide receptor.";
Nature 338:78-83(1989).
                                                                                                                                                             Chinkers M., Garbers D. Goeddel D.V., Schulz S.
                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                  A-type receptor).
                                     SEQUENCE FROM N.A MEDLINE-91352095;
                                                                                                                 SEQUENCE FROM
                                                                                                                                                                               MEDLINE-89143770;
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                                                                                                                                                                                                                     NCBI_TaxID=10116;
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TQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAESTP
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ers D.L., Chang M.S.,
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Rodentia;
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41.9%;
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Pred. No. 2.
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| natriuretic peptide
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Murinae; Rat
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Matches 1
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DOMAIN
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Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00255; NATPEPTIDER.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entities requires a license content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYCLASE ACTIVITY ON BINDING OF ANF.

- CAPALYTIC ACTIVITY: GTP = 3',5'.cyclic GMP + diphosphate.

- SUBCELLIULAR LOCATION: Type I membrane protein.

- I MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00458; ANF_RECEPTORS; 1
PROSITE; PS00452; GUANYLATE_CYCLASS
PROSITE; PS50125; GUANYLATE_CYCLASS
PROSITE; PS50011; PROTEIN_KINASE_DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X14773; CAA32881.1; -. EMBL; J05677; AAA41200.1; -. EMBL; M74535; AAA41202.1; -. EMBL; S03348; OYRTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Trans cGMP synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001177; Ntpep_receptorN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - I - SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 88:7882-7886(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q02846;
                                                                                              Similarity
                    DGLKKRL----GKLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFS 478
DNLLSRMEQYANNLEELVEERTQAYLEEKRKAEALLYQILPHSVAEQLKRGETVQAEAFD 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Phosphorylation; Lyase
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192
451
460
                                                                             Conservative
                                                                                                                                                          AA;
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GUANYLATE_CYCLASES_2; 1.
PROTEIN_KINASE_DOM; 1.
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44.98;
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INTERCHAIN (PROBABLE).
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                         Score 457.5; DB 1; Pred. No. 3.9e-24; 0; Mismatches 78;
                                                                                                                                                                           N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
Q -> H (IN REF. 3).
L -> P (IN REF. 3).
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BY SIMILARITY.
BY SIMILARITY.
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POTENTIAL.
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Search completed: June 27, 2003, 13:03:26 Job time: 13.0695 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07; Search time 9.93048 Seconds (without alignments) 2585.358 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-762-767A-4
3231
1 MYGFVNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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MEDLINE-92316204; PubMed-1352257; Giulil G., Scholl U., Bulle F., Guellaeen G.; Milli G., Scholl U., Bulle F., Guellaeen G.; Molecular cloning of the cDNAs coding for the two subunits of soluble guanylyl cyclase from human brain."; EBS Lett. 304:83-88(1992). TISSUE-Kidney; Gansemans Y., Brouckaert P., Fiers W.; Submitted (AUG-1997) to the EMEL/GenBank/DDBJ databases. [3] SEQUENCE OF 337-545, AND ALTERNATIVE SPLICING. TISSUE-lung; MEDLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; PubMed-1680753; Chajilani V., Fraendberg PA., Ahlner J., Axelsson K.L., MILLINE-92008652; MEDLINE-92008652; MEDLINE-92	1 5

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Guanylate cycla
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Ffam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCc; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

Lyase; CGMP Synthesis; Alternative splicing.

Lyase; CGMP Synthesis; Alternative splicing.

DOMAIN 421 554 GUANYLATE CYCLASE.

VARSPLIC 393 425 MISSING (IN ISOFORM HSGC-2).

SEQUENCE 619 AA; 70514 MW; 231E4E660DE02AA1 CRC64;
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(Rel. 14, Last sequence update)
(Rel. 40, Last annotation update)
yclase soluble, beta-1 chain (EC 4
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PIR; SOLO3; OYBO70.

PDB; 1AWN; 28-JAN-98.

InterPro; IPRO01054; G_cyclase.

Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

SMART; SM00042; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

LYASS; CGMP SYNTHESIS; 3D-STRUCTURE.

DOMAIN

421 554 GUANYLATE CYC
SEQUENCE 619 AA; 70502 MW; 8EFB14952BE
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GUCYIB1 OR GUCIB3.

Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-Lung; MEDLINE-89031214;
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a comment the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is liftled and this statement is not removed. Usage by and foilties requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
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613; Conser
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S01653; OYBO70.
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X MEDLINE-89087429; PubMed-2905128;

XA MAKANE M., Saheki S., Kuno T., Ishii K., Murad F.;

AN ANAKANE M., Saheki S., Kuno T., Ishii K., Murad F.;

White M., Saheki S., Kuno T., Ishii K., Murad F.;

White M., Saheki S., Kuno T., Ishii K., Murad F.;

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White M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M., Milling M
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-1 chain (EC 4
(Soluble guanylate cyclase small subunit).
GUCYIB1 OR GUCYIB3 OR GUCYIB3.
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      EMBL; M22562; AAA41204.1;
PIR; A31871; OYRTB1.
HSSP; P16068; 1AWN.
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Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                      Lyase; cGMP synthesis.
DOMAIN 421 554
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              LNAGEILQMFGKMFFVFCQESGYDTILRVLGSNVREELQNLDALHDHLATIYPGMRAPSF
                                                                                                                                                                                                                                                                                                                                     TVSGLPEPCIHHARSICHLALDMMEIAGQVQVDGESVQITIGIHTGEVVTGVIGQRMPRY
                                                                                                                      RCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL
VWFLSRKNTGTEETKQDDD
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SULT 4

CYG2_RAT STANDARD; PRT; 682 AA.

CYG2_RAT STANDARD; PRT; 682 AA.

P22717;

01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, beta-2 chain (EC 4.6.1.2) (GCS-beta-2).

GUCY1B2.

Rattus norvegious (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattles nocregious (Rat).

SEQUENCE FROM N.A.
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Query Match
Best Local (
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InterPro; IPR001230; Prenyl_site.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. between the Swiss Institute of Bio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 29:10872-10878(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new form of guanylyl cyclase is preferentially expressed in
kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Kidney;
MEDLINE-91105012; PubMed-1980215;
Yuen P.S.T., Potter L.R., Garbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A36228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. SUBCELLULAR LOCATION: CYCOPLASMIC.
TISSUE SPECIFICITY: KIDNEY AND LIVER.
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CY
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GU
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE
MAGNESIUM OR MANGANESE IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E; PS50125,
IE; PS50125,
2; CGMP synthesis.
408 536 GU
     413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M57507; AAA41207.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                            GNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTEISCLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILQMFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSFRCTDA
     DVVTFTNIC:
                                   GIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGL
                                                                          SCQLERKKEELRVLSNHLAIEKKKTETLLYAMLPEHVANQLKEGRKVAAGEFETCTILFS
                                                                                                                                                   LKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQFREEYKL 365
                                                                                                                                                                                                                             QKFALDEYFSIIHPQVTFNISSICKFINSQFVLKTRKEMMPKAR-----KSQPMLK
                                                                                                                                                                                                                                                                                                                                                                                                                         LIEEKESKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG-AMLLHYYSDRHGLCHIVPGIIEAVAKDFFDTDVAMSILDM-NEEVERTGKKEHVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEEC-----DHTQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILKLEGEYFFKECKMSGYDRMLRTLGGNLTEFIENLDALHSYLALSYQEMNAPSFRVEEG
                                                                                                                                                                                                                                                                                                      SVLFGKGPLRDTFQPVYPERLWVEEEVFCDAFPFHIVFDEALRVKQAGVNIQKYVPGILT
                                                                                                                                                                                                                                                                                                                                                                                LVVQKAHRQIRGAKASRPQGSEDSQADQEALQGTLLRMKERYLNIPVCPGEKSHSTAVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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AACE-PIQIVMLNSMYSKFDRLTSVHD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO ADENYLYL CYCLASE CLASS-4/GUANYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 987; DB
Pred. No. 1.4e
04; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUANYLATE CYCLASE. 98C173C1A1CC7715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ght. It is produced through Bioinformatics and the EN titute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF GUANYLATE CYCLASES:
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.4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
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- outstation
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RESULT 5
CYG2_HUMAN
ICYG2_HUMAN
ICYG2_HUMAN
ICYG2_HUMAN
ICYG2_HUMAN
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075343; Q9N:
AC 075345; AC 075345; AC 075345; AC 075345; AF 07535; 
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                                               InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1999 (Rel. 38, Creat
16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Guanylate cyclase soluble,
                                                                                                                                                                            EMBL; AF038499; AAD09440.2;
EMBL; AF218383; AAF66105.1;
HSSP; P19687; IAWN.
                                                                                                                               MIM; 603695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Behrends S., Kazmierczak B., Steenpa A., Knauf B., Bul
Scholz H., Elberg H.;
"Assignment of GUCIH2, the gene coding for the beta2
guanylyl_cyclase to chromosomal band 13q14.3 between m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 55:126-127(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                guanylyl cyclase to
and D13S155.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The beta(2) subunit of soluble guanylyl cyclase contains human-specific frameshift and is expressed in gastric card Biochem. Biophys. Res. Commun. 271:64-69(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99107820; PubMed-9889008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Behrends S., Vehse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20241821; PubMed=10777682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.

MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMERANE-ASSOCIATED RECEPTOR FORMS.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: GTP = 3',5'-cycli
ENZYME REGULATION: ACTIVATED BY NITRI
MACHESIUM OR MANGANESE IONS.
SUBUNIT: HETERODIMER OF AN ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580
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                                                                                                                                                    HGNC:4686;
  PS00452; GUANYLATE_CYCLASES_1; PS50125; GUANYLATE_CYCLASES_2;
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Primates;
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annotation update)
beta-2 chain (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3',5'-cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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  FALSE_NEG
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IN THE PRESI
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RESULT 6
CYC4_CYC1
ID CYC4A
AC Q9WW
AC Q9WW
AC Q9WW
AC GUAN
GUCY
OS RATT
OX NCBL
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
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DOMAIN
"Cloning and functional expression of the rat alpha(2) subunsoluble guanylyl cyclase.";

Biochim. Biophys. Acta 1494:286-289(2000).

-!- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1:
-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate
-!- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRES!
                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Wistar Kyoto; TISSUE-Aorta;
MEDLINE-20571097; PubMed-11121588;
                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
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nilarity 36.6%;
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40, Last sequence update,
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• soluble, alpha-2 chain (EC
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Rodentia;
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Sciurognathi; Muridae;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
Lyase; CGMP synthesis; Multigene family
DOMAIN 519 646 GUANYLATE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF109963; AAD42949.2; -. HSSP; P19687; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
 658
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                                                               NLDDLTRRGLYLSDIPLHDATRDLYLLGEQFREEYKLTQELEILTDRLQLTLRALEDEKK
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A variant of the alpha 2 subunit of soluble guanylyl cyclase grounding on thin and insert homologous to a region within adenylyl cyclases and functions as a dominant negative protein.";

L. J. Biol. Chem. 270:21109-21113(1995).

C. I- FUNCTION: HAS GUANYLYL CYCLASE ON BINDING TO THE BETA-1 SUBUNITS C. I- FUNCTION: HAS GUANYLYL CYCLASE ACTIVITY AS IT FORMS NON-FUNCTION HETERODIMERS WITH THE BETA SUBUNITS.

C. I- CATALYIK ACTIVITY: GTP - 3',5'-cyclic GMP + diphosphate.

C. I- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN THE PRESENCE OXIDE IN FETAL BRAIL INTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) AND ALPHA-2-1; ARE PRODUCED BY ALTERNATIVE SPLICING.

C. INTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) AND ALPHA-2-1; ARE PRODUCED BY ALTERNATIVE SPLICING.

C. INTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2 (SHOWN HERE) IN FETAL BRAIL INVEX, COLON AND ENDOTHELIUM.

SEXPRESSED ONLY IN LIVEX, COLON AND ENDOTHELIUM.

C. INTERNATIVE SECURIORS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE.
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PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
Lyase; CGMP synthesis; Multirene family; Alternative DOMAIN 51 648 GUANYLATE CYCLASE.
DOMAIN 51 76 ALA-RICH.
DOMAIN 51 58 POLY-ALA.
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EMBL; Z50053; CAA90393.1;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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P19686;
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC
(Soluble guanylate cyclase large subunit).
GUCY1A1 OR GUC1A1.
                                            Nakane M., Aral K., Saheki S., Kuno T., Bue "Molecular cloning and expression of cDNAs guanylate cyclase from rat lung.";
J. Biol. Chem. 265:16841-16845(1990).
                                                                                                                                              MEDLINE=91009100;
                                                                                                                                                                                       SEQUENCE FROM N.A.,
    SEQUENCE
                                                                                                                                                                    TISSUE-Lung;
                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                             Rattus norvegicus
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79465A7D3FE52DB7 CRC64;
                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
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MEDLINE-97151325; pubmed-8997507;
Smigrodzki R.M., Levitt P.;
Smigrodzki R.M., Levitt P.;
The alpha I subunit of soluble guanylyl cyclase is prenatally in the rat brain.";
Brain Res. Dev. Brain Res. 97:226-234(1996).
-i- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + dip
-i- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN
MAGNESIUM OR MANGARESE IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M57405; AAA41206.1; -. EMBL; U60835; AAB17953.1; -. PIR; A38297; OYRTA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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SUBCELLAUGAR LOCATION: CYCOPLASMIC.
MISCELLAUGUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES:
FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
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FTAICSQCS----PLQVITMLNALYTRFDQQCGELD---VYKVETIGDAYCVAGGLHRES
                                              FNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPC
                                                                                                GKLKATLEHAHQALEEEKKKTVDLLCSIFPSEVAQQLWQGQIVQAKKFNEVTMLFSDIVG
                                                                                                                             EILTDRIQLTLRALEDEKKKTDTLLYSYLPPSVANELRHKRPVPAKRYDNVTILFSGIVG
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480 607 GUANYLATE CYCLASE.
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EMBL; X66534; CAA47145.1; -.
EMBL; U58855; AAB94794.1; -.
EMBL; Y15723; CAA75738.1; -.
PIR; S23098; S23098.

P19687; HGNC:4685;

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RESULT 9
CYG3_HUMAN
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"Human soluble guanylate cyclase: functional expression and revision is sonzyme family.";

It soonzyme family.";

Biochem. J. 335:51-57(1998).

C -!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C -!- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE MAGNESIUM OR MANGANESE IONS.

C -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -!- SUBCELLAULAR LOCATION: Cytoplasmic.

C -!- MISCELLAULAR LOCATION: Cytoplasmic.

C -!- MISCELLAUGHS THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOL FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

C -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCL
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2)
(Soluble guanylate cyclase large subunit) (GCS-alpha-1)
GUCYIA1 OR GUCYIA3 OR GUCYIA3 OR GUCYIA3.
                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Kidney;
Gansemans Y., Brouckaert P., Fiers W.;
"Human soluble guanylate cyclase large subunit mRNA,
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92316204; PubMed-1352257; Giuili G., Scholl U., Bulle F., Guellaeen G. "Molecular cloning of the cDNAs coding for t soluble guanylyl cyclase from human brain."; FEBS Lett. 304:83-88(1992).
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Mammalia; Eutheria;
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     CONFLICT
CONFLICT
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PROSITE; PS0125; GUANYLATE_CYCLASES_2; 1.
Lyase; CGMP synthesis; Multigene family.
DOMAIN 481 608 GUANYLATE CYCLASE.
CONFLICT 124 127 AAGY -> QQS (IN RE CONFLICT 131 184 VIKESLGEEVFKICYEEI
(Solub)
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AAGV -> QQS (IN REF. 1).
VIKESLÆEEVRKICYEBEDENILGVVGGTLKDFLNSFSTLLK
QSSHCQEAGKRGR -> LSKNLLVKRFLKYVTRKMKTSLGW
LEAPLKIFKQLQYPSETEQPLPRSRKKGQ (IN REF.
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Pred. No. 5.8e-47;
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GDAYCYA -> AMPIWHL (IN REF. 1).

GNANFLYKAGGID -> ASOPERQSIENRLATYIPIYKSLG

FDSLKMCRASESTLGIVDG (IN REF. 1).
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D-STRUCTURE MODELING OF 472-628.

MEDLINE-98054247; PubMed-9391039;

A Liu,Y., Ruoho A.E., Rao V.D., Hurley J.H.;

MICHAELYTIC mechanism of the adenylyl and guanylyl cyclases: model "Catalytic mechanism of the adenylyl and guanylyl cyclases: model and mutational analysis.";

T proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).

C -!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

C -!- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE MAGNESIUM OR MANGANESE IONS.

C -!- SUBURIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -!- SUBCELIULAR LOCATION: Cytoplasmic.

C -!- MICCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOL FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

C -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.

Lyase; cGMP synthesis; Multigene family; 3D-structure.

DOMAIN

482

609

GUANYLATE CYCLASE

GUANYLATE CYCLASE

SEQUENCE 691 AA; 77532 MW; 5D1FE4D2204E8683 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
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MEDLINE-90306336; PubMe
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X54014; CAA37960.1;
S10713; OYBO77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                     KEAQLDEEGGFLVRIIYDDSKTYDLVAAASKVLNLNAGEIL-QMFGKMFFVFCQESGYDT
                                                         DFYEDLDRFEENGTQ------
-FHQDCREFVDQPCELYSVHIRSARPHPPPGKPVSSLVIPASLFCKTFPFHFMLDRDMSI
                                                                                                                   VLYVYYFFPKRITSLILPGIIKAAARILYETEVEVSSTPSR
                                                                                                                                                                      -LILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFLIEEKESKEE
                                                                                                                                                                                                                                                                                             ILRVLGSNVREFLQNLDALHDHLATIYPGMRAPSFRCTDAEKGKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 770;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                -LKQSSHCQEAEK-KGRFEDASILCLDKDPD
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..3e-45;
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                                                                                                                                                                                                                                                                                                                               007093;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Head-specific guanylate cyclase (EC 4.6.1.2).
GYC-ALPHA-994 OR GYC-ALPHA-63A OR GYC OR DGC1.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
Insecta; Ephydroidea; Drosophilidae; Drosophila.
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Canton-S; TISSUE-Head;
MEDLINE-93203896; PubMed-8095978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
                                                                                                                                                                                                                     J. Neurochem. 60:1570-1573(1993).
                                                                                                                                                                                                                                             "Isolation of a Drosophila gene encoding a cyclase.";
                                                                                                                                                                                                                                                                   Yoshikawa S., Miyamoto Mikoshiba K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYGH_DROME
                       EMBL;
                                                                                                                                          SUBUNIT: DIMER (PROBABLE).
SUBCELLULAR LOCATION: CYCOPLASMIC (Potential).
TISSUE SPECIFICITY: HEAD, WHERE IT IS PREFERENTIALLY EXPRESSED IN THE CNS AND THE RETINA. NOT FOUND IN BODIES.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE.
                                                                                                                                                                                                 MAY BE REQUIRED FOR ENZYME ACTIVITY.
CATALYTIC ACTIVITY: GTP = 3',5'-cyclic
 ; S57126; AAB25820.1;
JH0810; JH0810.
; P19687; LAWN.
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Query Match
Best Local :
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PROSITE: PS00452; GUANYLATE_CYCLASES_1; FALSE_N
PROSITE: PS50125; GUANYLATE_CYCLASES_2; 1.

Lyase: CGMP synthesis; Multigene family; Vision
Lyase: CGMP synthesis; Multigene family; CYCLASE.

DOMAIN

465

591
                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Atrial natriuretic peptide receptor A precursor (Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0013972; Gyc-alp
InterPro; IPR001054; G_cyclas
Pfam; PF00211; guanylate_cyc;
SMART; SM00044; CYCC; 1.
   Eukaryota;
Mammalia;
                                              A-type receptor).
NPR1 OR ANPRA.
                                                                                                                                                                 ANPA_HUMAN P16066;
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                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                   LPKEFP-----
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 ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                KGKKEPMQVWFLSRKNTGTEET
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                                                                                                                                                                                  STANDARD;
Chordata;
Primates;
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Pred. No. 1.3e-41;
Craniata; Vo
Catarrhini;
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Vertebrata;
i; Hominidae;
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| natriuretic peptide
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the European use by non-profit institutions as modified and this statement is not removed entitles requires a license agreement (See an an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              CYCLASE ACTIVITY ON BINDING OF ANF.

-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP +

-!- SUBCELLULAR LOCATION: Type I membran-
                      EMBL;
EMBL;
EMBL;
EMBL;
                                                                               EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclase (ANPRA) in human retina.";
Cell. Mol. Neurobiol. 14:1-7(1994)
-1- FUNCTION: RECEPTOR FOR ATRIAL N
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Takahashi Y., Nakayama T., Soma M., Izumi Y., Kanmatsuse K.;
"Organization of the human natriuretic peptide receptor A gene.";
Biochem. Biophys. Res. Commun. 246:736-739(1998).
                                                                                                                                                     EMBL;
                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of functhe human """
                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pardhasaradhi K., Kutty R.K., Gentleman S., "Expression of mRNA for atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 634-1048 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human atrial natriuretic peptide receptor defines a
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                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIECULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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AB010472;
AB010474;
AB010475;
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AB010477;
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AB010481;
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M.S., Hellmiss R.,
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tic peptide receptor A gene.";
) to the EMBL/GenBank/DDBJ databases.
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: peptide r
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Best Local
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Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF00211; guanylate_cyc; 1.

Pfam; PF00194; ANF_receptor; 1.

PRINTS; PR00255; NATPEPTIDER.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00458; ANF_RECEPTORS; 1.

PROSITE; PS00458; GUANYLATE_CYCLASES_1; 1.

PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
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EMBL; AF190631; AAF01340.1;
EMBL; S72628; AAD14112.1; -
PIR; S04459; OYHUAR.
HSSP; Q02846; IAWL.
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InterPro; IPR000719; Euk_Pklnase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_receptorN.
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   TRRGLYLSDIPL----
                                  ITDYGLESFRDLDPE----
                                             DWMFRYSLINDIVKGMLFLHNGAICS
                                                                                                                    IEL--TRKVLFELKHMRDVQNEHLTRFVGACTDPPNICILTEYCPRGSLQDILENESITL
                                                                                                                                         EECDHTQFLIEEKESKEEDFYEDLDRFEENGTQESRISPYT-FCKAFPFHIIFDRDLVVT
                                                                                                                                                              --RSAGSRUTLSGRGSNYGSLL---TTEGQFQV---FAKTAYYK--GNLVAVKRVNRKR
                                                                                                                                                                                    GMRAPSFRCTDAEKGK--GLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRN
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876
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           CYCLASE ACTIVITY ON BINDING OF ANF.

-! CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
-!- SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
-!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                               MEDIINE-91352095; PubMed-1679239;
Duda T., Goraczniak R.M., Sharma R.K.;
"Site-directed mutational analysis of a membrane guanylate cDNA reveals the atrial natriuretic factor signaling site."
Proc. Natl. Acad. Sci. U.S.A. 88:7882-7886(1991).
-I- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS
                                                                                                                                                                                                                                                                                                                Goeddel D.V., Schulz S.;
"A membrane form of guanylate cyclase peptide receptor.";
Nature 338:78-83(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
                                                                                                                                                                                                                              Yamaguchi M., Rutledge L.J., Garbers D.L.;
"The primary structure of the rat guanyly!
natriuretic peptide receptor gene.";
J. Biol. Chem. 265:20414-20420(1990).
                                                                                                                                                                                                                                                                    MEDLINE=91056089; PubMed=1978722;
Yamaguchi M., Rutledge L.J., Garb
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Goeddel D.V., Schulz S.;
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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01-NOV-1990
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CARBOHYD
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PTODOM; PD000001; EUK_PKINASE; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS00458; ANE_RECEPTORS; 1.

PROSITE; PS00452; GGANYLATE_CYCLASES_1;

PROSITE; PS50125; GUANYLATE_CYCLASES_2;

PROSITE; PS50111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X14773; CAA32881.1; -.
EMBL; V05677; AAA41200.1; -.
EMBL; M74535; AAA41202.1; -.
PIR; S03348; OYRTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001054; G_c
InterPro; IPR001170; Ntp
Pfam; PF002011; guanylate
Pfam; PF00211; guanylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
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                                                                            VVSGLP---VRNGQLHAREVARMALALLDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGVV
                                         GQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLEHRGPVSMK
                                                                                                TVSGLPEPCIH----HARSICHLALDMMEIAGQVQV---DGESVQITIGIHTGEVVTGVI
                                                                                                                                    TIYFSDIVGFTALSAEST----PMQVVTLLNDLYTCFDAVID---NFDVYKVETIGDAYM
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                           GLKMPRYCLFGDTVNTASRMESNGEALKIHLSSETKAVL--
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Euk_pkinase.
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GUANYLATE CYCLASE.
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INTERCHAIN (PROBABLE).
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RESULT 14
ANPA_MOUSE
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS: PR00255; NATPEPTIDER.
ProDom; PD000001; Euk_pkinase; 1.
SMARF; SM00444; CYCC; 1.
PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00459; GOANYLATE_CYCLASES_1; 1.
PROSITE; PS0159; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                               EMBL; J05504; AAA37670.1; -
EMBL; L31932; AAA65945.1; -
PIR; A35568; OYMSAR.
PIR; A33088; A33088.
HSSP; Q02846; LAWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95139994; PubMed-7838126; Schoenfeld J.R., Sehl P., Quan C., Burr Agonist selectivity for three species receptor-A.";
                                                                                                                                                                                  MGD; MGI:97371; Npr1.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001054; G_cyclase.
InterPro; IPR001170; Ntpep_recepto
                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Mus musculus (Mouse).

Mus musculus (Mouse).

Charvots; Metazoa; Chordata;

Charvota; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pandey K.N., Singh S.; "Molecular cloning and expression of murine guanylate cyclase/atrial natriuretic factor receptor cDNA."; J. Biol. Chem. 265:12342-12348(1990).
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NCBI_TaxID=10090;
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CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWAITH GUANYLATE CYCLASE ACTIVITY (AMP-A AND ANP-B) AND ONE (AMP-GWITCH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AMP FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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(Rel. 40, Last annotation update)
iuretic peptide receptor A precursor (ANP-A) (ANPRA) (GC-A)
cyclase) (EC 4.6.1.2) (NPR-A) (Atrial natriuretic peptide
                                                                                                                                                                     pkinase;
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Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
                                                                                                                                                                                                                                                       251
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NAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCI
                                         LVEERTQAYL----EEKRKAEALLYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGF
                                                                FNKENSSNI
                                                                                                                                                                                                                                                  LSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTEISCLRLKGQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFAKTAYYKGNLVAVKRVNRKRIELTRKVLFELKHMRDVQNEHL-TRFVG-----ACTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFCQESGYD----TILRVLGSNV---REFLQNL----DALHDHLATIYPGMRAPSFRCTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYRKMQLEKELVSELWRVRWEDLQPSSLERHLRSAGSRLTLSGRGSNYGSLLTTEGQ-FQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKKEAQLDEE-GOFLVRIIYDDSKTYDL---VAAASKVLNL----NAGEILQMFGKMFF
                                                                                                                                                                 IYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVLLGEQFREEYKLTQELE
                                                                                                                                                                                                                                                                                                                                                                                SSNCVVDGRFVLKITDYGLESFRDPEPEQGHTLF-----AKKLWTAPELLRMASPPARG
                                                                                                                                                                                                                                                                                                                                                                                                                          -----TEIDMKVIQQRNEECDHTQFLIEEKESKEEDFYEDLDRFEE---NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEKGKGLILHYYSEREGLQDIVIG------
                                                                                                                                                                                                           ----FRPSMDLQ-----SHLEELGQL------MQRCWAEDPQERPPFQQIRLALRK
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5; Mismatches
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
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.1e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 182;
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(POTENTIAL).
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RESULT 15
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P16067;
01-APR-1990
                               Pfam;
Pfam;
                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-89376566; Pul Schulz S., Singh S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Atrial natriuretic peptide receptor B precursor (ANP-B) (ANPRB) (GC-B)
(Guanylate cyclase) (EC 4.6.1.2) (NPR-B) (Atrial natriuretic peptide
                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                      InterPro;
                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116
                                                                                                                                InterPro;
                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e primary structure of a plasma membrane guanylate cyclase constrates diversity within this new receptor family.";

1 58:1155-1162(1989).

1 58:1155-1162(1989).

FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMULATED MORE. EFFECTIVELY BY BRAIN NATRIURETIC PEPTIDE (BMP) THAN BY ANP. CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANEOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO MITH GUANYLATE CYCLASE ACTIVITY (AMP-A AND ANP-B) AND ONE (AMP-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC DOMAIN OF PROTEIN KINASES.
SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASI
                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1048
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                             PF00211;
PF01094;
                                                                     PF00069;
                                                                                                                                                                      Q02846;
                                                                                                                                                                                                              м26896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :: | ::| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
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                                                                               IPRO01828; ANF_receptor.
IPRO00719; Euk_pkinase.
IPRO01054; G_cyclase.
IPR001170; Ntpep_receptorN.
                                                                                                                                                                                                              AAA41205.1; -.
                           guanylate_cyc; 1.
ANF_receptor; 1.
                                                                   pkinase;
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PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
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RCLMSPENSDPQFHLEHRGPVSMKGKKEPMQVWFLSRK
                                                            YTRFDTLTDSRKNPFVYKVETVGDKYMTVSGLP-EPCIHHARSICHLALDMMEIAGQVQV 512
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                                                                                                                                                                                                                          LYQILPHSVAEQLKRGETVQAEAFDSVTIYFSDIVGFTALSAEST----PMQVVTLLNDL
                                                                                                                                                                                                                                                                                                          TERPDFGQIKGFIRRFNKEGGTSILDNLLLRMEQYANNLEKLVEERTQAYLEEKRKAEAL
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114

453 833 393 773 357 717 304 657 277 597

1007 DAL----DELGCEQLELRGDVENKGKGKMRTYWLLGER 1040

Search completed: June 27, 2003, 13:03:29 Job time: 12.9305 secs

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OM protein - protein search, using sw model
                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: June 27, 2003, 13:00:58; Search time 31.2101 Seconds (without alignments) 4086.601 Million cell updates/sec

Title: Perfect score:

Sequence:

US-09-762-767A-4
3231
1 MYGFVNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:* sp_archea:*
sp_bacteria:*
sp_fungi:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_phage: * sp_organelle:* sp_plant:*
sp_rodent:*

sp_virus:*

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2		Result
914	929.5	938	955	955	960.5	983	1105	1761	1870.5	1883	1883	1903.5	2859	2887	3198	Score
28.3	28.8	29.0	29.6	29.6	29.7	30.4	34.2	54.5	57.9	58.3	58.3	58.9	88.5	89.4	99.0	Query Match
699	690	751	940	686	. 685	636	742	649	604	787	758	600	617	614	620	Query Match Length DB
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	Q9vfc5 drosophila	002298 caenorhabdi	076340 manduca sex	P92006 caenorhabdi	Q9xteO caenorhabdi		7	Q17010 anopheles g	Q95nk5 hemicentrot	Q9va09 drosophila	Q24086 drosophila	077106 manduca sex	Q90vy5 fugu rubrip	P79998 oryzias lat	O54865 mus musculu	Description

Query Match

99.0%; Score 3198; DB 11; Length 620;

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
456.5	458	464	466	467.5	469.5	470	471	472	478.5	490.5	493	565	646.5	685	701.5	704.5	720	726	729.5	757	778	778	778	783	786.5	788	788	912.5
14.1	14.2	14.4	14.4	14.5	14.5	14.5	14.6	14.6	14.8	15.2	15.3	17.5	20.0	21.2	21.7	21.8	22.3	22.5	22.6	23.4	24.1	24.1	24.1	24.2	24.3	24.4	24.4	28.2
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	α	Q9pwh0 xenopus lae	4	a	Q90yb7 rana catesb	Q18331 caenorhabdi	oryzias	Q98uil oryzias lat		093490 anguilla ja	4		P90895 caenorhabdi	Q9veu6 drosophila			Q95sq4 drosophila			3	Q9erl9 mus musculu		P79997 oryzias lat	Q9pwi2 oryzias lat	Q8tah3 homo sapien	Q90vv5 fugu rubrip	Q9nnw8 homo sapien	Q9bi80 caenorhabdi

ALIGNMENTS

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                                                                         "Molecular cloning of cDNAs and exprebeta subunits of soluble guanyl"

latipes.";

Eur. J. Bloch-"
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Soluble guanylyl cyclase beta subunit (EC 4.6.1.2).
Oryzias latipes (Medaka fish).
Cryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleose
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleo
Acanthomorpha; Acanthopterygii; Percomorpha; Atherlnomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
NCBI_TaxID=8090;
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SEQUENCE FROM
                             SEQUENCE FROM N.A. MEDLINE-99303623;
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Q90VY5 PRELIMINARY; PRT; b1/ AA. Q90VY5; Created)
01-DEC-2001 (TIEMBLIEL 19, Last sequence up-
01-MAR-2002 (TIEMBLIEL 20, Last annotation -
Soluble guanylyl cyclase betal subunit.
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Mikami T., Kusakabe T., Suzuki N.;

"Tandem organization of medaka fish solu
and betal subunit genes. Implications for
two subunit genes.",
J. Biol. Chem. 274:18567-18573(1999).
EMBL; AB000850; BAA19199.1;
EMBL; AB022281; BAA76691.1;
HSSP; P1668; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001054; G_cyclase.
pfam; pF0021; guanylate_cyc; 1.
SMARP; SM00044.-CYCc; 1.
PROSITE; PS00452; GUANYLATE_CYCL
PROSITE; PS50125; GUANYLATE_CYCL
                                                                                                                                                                                                                                                                                                                                                                                    11 Similarity 89.7
547; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T., Kusakabe T.,
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PS00452; GUANYLATE_CYCLASES.
PS50125; GUANYLATE_CYCLASES.
         VWFLSRKNTGTEE
                               PQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTE
VWFLSRKSSDADK
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Pred. No. 9
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hes 29;
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Best Local S
Matches 540
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AB062172; BAB60908.1; -.

REMBL; AB062170; BAB60906.1; -.

RINTELPTO; IPR001054; G_Cyclasse.

RINTELPTO; IPR0001054; G_Cyclasse.

RINTELPTO; IPR00010834; Zn_carbopept.

REMBL; AB06217; Guanylate_cyc; 1.

RPROSITE; PS00132; CARBOXYPEPT_ZN.1; UNKNOWN_1.

RROSITE; PS00132; CARBOXYPEPT_ZN.1; UNKNOWN_1.

RROSITE; PS00132; GUANYLATE_CYCLASES_1; UNKNOWN_1.

RROSITE; PS0152; GUANYLATE_CYCLASES_2; 1.

SEQUENCE 617 AA; 70236 MW; 7B531B5896A06191 CRC64;
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Frugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morinaga C., Yamamoto T., Moriya Y., Suzuki N.; 
"Identification of tandem organization of soluble
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VWFLSRKNT
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                                                                                                      RCTDAEKGKGLILHYYSEREGIQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL
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41; Mismatches
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1.3e-207;
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O77106;
O1-NOV-1998 (TIEMBLICEL 08, Created)
O1-NOV-1998 (TIEMBLICEL 08, Last sequence update)
O1-NOV-1998 (TIEMBLICEL 20, Last annotation update)
O1-MAR-2002 (TIEMBLICEL 20, Last annotation update)
Soluble guanylyl cyclase beta-1 subunit.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; D1
Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
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MEDLINE-98409773; PubMed-9736646;

Nighorn A., Gibson N.J., Rivers D.M., Hildeb

"The nitric oxide-cGMP pathway may mediate c
sensory afferents and projection neurons in
manduca sexta.";
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EMBL; AF062751; AAC61264.1; -.
HSSP; P16068; 1AWN.
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Pred. No. 2.1e-1
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138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Two Drosophila genes that encode the alph brain soluble guanylyl cyclase.";
J. Biol. Chem. 270:15368-15376(1995).
EMBL; U27123; AAA87941.1; -.
HSSP; P16068; 1AWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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SMART; SM00044; CYCC; 1.
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Ephydroidea; Drosophi
NCBI_TaxID=7227;
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            ELTGTEISCLRLKGQMIYLPEADSILFLCSPSVMNLDDLTRRGLYLSDIPLHDATRDLVL
                                                                                                                                                                                                        NNNDGQQIASETDPSIALSTCPIAQDSFDCDGDKEQKCLRLLKNKSDDIERYDHVQFLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYGFVNYALELLVLKHFGEEIWEKIKKKAMVSMEGQFLVRQIYDDEITYNLIGAAVEILN
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                                                  AVSRVIPRVAEENCSLIEVVEAIRPHLQLNFENILSHINTIYVLQTRQGAMS
                                                                                    AIYRVLPQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECED
                                                                                                                            EINVAAKSQVDAKKDEVPDDMEFL----CEAPLISPATFCKVFPFHLMFDRQMKIVQAGK
                                                                                                                                                                                                                                                                                     RAIARENQQLLEDAVATTTTGSATVVLAPSSDAERNNHHNGSNGSNNNGMANNGNTVNVN
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OR DGCB1 OR CG1470.
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                                                                                                                                                              -KESKEEDFYEDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84444 MW;
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2; Mismatches 12
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.;
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Chambios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Merson D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Syles B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Syles B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
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GYC-BETA-100B OR GYCBETA100B OR CG1470.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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KRYDNYTLMFSGIVGFGQYCAANTDPDGAMKIVKMLNELYTVFDALTDSKRNLNVYKVET
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Matches 371
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EMBL; AE003777; AAR57119.1; -.
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InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMARP; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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KRYDSYTLMFSGIVGFGQYCAANTDPDGAMKIVKMLNELYTVFDALTDSKRNLNVYKVET
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                                                                                                                                                                                                                           RCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNE------
KPTPMDCWFLTRATSSILGGTSST
               KKEPMQVWFLSRKNT----
                                                                                                                                                             --SRHEQRELRLKGQMMYIPETDRILFQCYPSVMNLDDLTKKGLYISDVPLHDAARDLYL
                                                                                                                                                                      AVSRVIPRVAEENCSLIEVVEAIRPHLQLNFENILSHINTIYVLQTRQGAMS-----
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EMBL; AB062380; BAB58877.1; JOINED.
EMBL; AB062380; BAB58877.1; JOINED.
EMBL; AB062380; BAB58877.1; JOINED.
EMBL; AB062380; BAB58877.1; JOINED.
EMBL; AB062386; BAB56135.1; JEMBL; AB062386; BAB56136; BAB56136; BAB56136; BAB56136; BAB56136; BAB56136; BAB56136; BAB56136; B
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Q95NK5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Soluble guanylyl cyclase betal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanabe Y., Suzuki N.;
"Genomic Structure and
Cyclase beta Subunit Ge
Submitted (MAY-2001) to
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PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
SEQUENCE 604 AA; 68198 MW; B1C79618705934D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemicentrotus pulcherrimus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                  RCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQFL
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                                                                                                              AKKFECVTLMFSGIFGFGDFCRRYS--HDAMKIVSLLNSVYTKFDVLMEN--NPDVYKVE
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57.2%;
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%; Pred. No. 6.7e-133;
112; Mismatches 126; 1
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RESULT Q17010

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Query Match
Best Local S
Matches 345
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EMBL; U42613; AAC47142.1; -.
EMBL; A017062; AAC47144.2; -.
EMBL; U42612; AAC47141.1; -.
EMBL; U42614; AAC47143.1; -.
HSSP; P16068; IAWN.
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SEQUENCE
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STRAIR-SUA, G3, GMMKG, AND MC;
MEDLINE-96400927; PubMed-8807303;
Garcia B.A., Caccone A., Mathiopoulos K.D.,
"Inversion monophyly in African anopheline i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q17010 PRELIMINARY; PRT; 649 AA. Q17010; Q17007; Q17008; Q17009; Q17009; Q17009; Q17009; Q17009; Q17009; Q17009; Q17009; Q17009; Q1, Created) Q1-NOV-1996 (TrEMBLrel. 12, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Soluble guanylyl cyclase beta subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00044; CYCC; 1.

PROSITE; PS00452; GUANYLATE_CYCLASES_1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCSBETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of the soluble guanylyl the mosquito Anopheles gambiae."; Insect Mol. Biol. 8:23-30(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSP; P160bb; Lam...
InterPro; IPR001054; G_cyclase.
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                       TAEPPVANTAAAATPKARHSIPEVVKSVPITSLDPAVPELANLGLCKRILASKTSSSGGP
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72514 MW;
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                                                                                                                                                                                                                                                                                                                                                            Score 1761; DB 5;
Pred. No. 1.4e-124;
4; Mismatches 116;
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malaria
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m vectors.";
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                                                                                                                                                Query Match
Best Local S
Matches 249
                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY;
MEDLINE-21391941; PubMed-11406623;
Koglin M., Vehse K., Budaeus L., Scholz H., Be
"Nitric Oxide Activates the beta 2 Subunit of
in the Absence of a Second Subunit.";
J. Biol. Chem. 276:30737-30743(2001).
EMBL; AV004153; AAF86581.1; -
InterPo; IPR001054; G_CyClase.
InterPo; IPR001230; Prenyl_site.
Pfam; PF00211; GUANYLATE_CYCLASES_1; UNKNOW
PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS00294; PRENYLATE_CYCLASES_2; 1.
PROSITE; PS00294; PRENYLATE_CYCLASES_2; 1.
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Q91XJ7;
Q91XJ7;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U1-DEC-2001 (TremBLrel. 19, Created)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-MAR-2002 (TremBLrel. 20, Last annotation update)
Soluble guanylyl cyclase beta 2 subunit.
GUCYIB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                Local Similarity
nes 249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                       61
                                                                                        MYGFVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN
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                                                                                                                                                  Conservative
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  :::
                                                                                                                                                                   34.28;
Score 1105; DB 11;
Pred. No. 6.6e-75;
7; Mismatches 221;
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e Guanylyl Cyclase
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                                            Query Match
Best Local Si
Matches 224;
                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLIFE1. 19, C:
01-DEC-2001 (TrEMBLIFE1. 19, L:
01-MAR-2002 (TrEMBLIFE1. 20, Lis
Soluble guanylate cyclase beta
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                             "CDNA cloning and expression analysis of novel v. beta2 subunit.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ da. EMBL; AB058888; BAB68564.1;

InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; UNKNOWN_PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.

SEQUENCE 636 AA; 71642 MW; 951DBDE8970E0890
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
Okamoto H., Asakawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              092001
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                                                             Similarity
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                                          30.4%;
ilarity 36.7%;
Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVTQCGNAIYRVL
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                                          Score 983; DB 11;
Pred. No. 8.9e-66;
4; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulsc Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M. Parsons J., Percy C., Rifken L., Roopra A., Saunders D. Smaldon N., Smith A., Sonnhammer E.
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01-NOV-1999
01-NOV-1999
01-JUN-2002
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Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
NCBI_TaxID=6239;
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InterPro; IPR001230; Prenyl_site.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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AL008867; CAM15512.1; -
Z99942; CAM15512.1; JOINED.
Q02846; IAWL.
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                                                                  NVSEYTYRCLMSPENSDPQFHLEHRGPVSMKGKKEPMQVWFLSR
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11; Mismatches 234
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P92006;
P92006;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
M04G12.3 protein.
M04G12.3.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCBL_TaxID-6239;
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SMART; SM00044; CYCC; 1.

PROSITE; PS00125; GUANYLATE_CYCLASES_2; 1.

PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

SEQUENCE 686 AA; 78588 MW; 65AE352DB53CBA57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001054; G_cyclase.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology ";
Science 282:2012-2018(1998).
EMBL; Z81103; CAB03210.1; -.
HSSP; P1606B; IAWN.
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PKNIVKLLNEVFFKLDRIVVLRG---
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MEDLINE-9910/914; PubMed-9891024;
Nighorn A., Byrnes K.A., Morton D.B.;
Nidentification and characterization of a
soluble guanylyl cyclase that is active in
subunit and is relatively insensitive to n
J. Biol. Chem. 274.2525-2531(1999).
EMBL; AF064514; AAD09836.1;
HSSP; Q02846; IAWL.
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O76340;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Soluble guanylyl cyclase beta-3.
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insect Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Sphingiodea; Sphingidae; Sphingidae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00211; guanylate_cyc; 1.

SMART; SM00044; CYCC; 1.

PROSITE; PS00095; C5_WTASE_2; UNKNOWN_1.

PROSITE; PS0125; GUANYLATE_CYCLASES_2; J

PROSITE; PS00294; PRENYLATION; UNKNOWN_1.

SEQUENCE 940 AA; 106393 MW; 08956886
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IPRO01054; G_cyclase.
IPR001230; Prenyl_site.
0211; guanylate_cyc; 1.
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
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Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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SEQUENCE FROM N.A.
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InterPro; IPR001230; Prenyl_sit
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Horst D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR001054; G_cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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                                                                                                                                                       RKNPFVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQVQ--VDGESVQITI
                                GVHSGAVVAGIVGLKMPRYCLFGDTVNTASRMESTSIAMKVHISEST-KVLIG----
                                                                                                                                                                                                                                                                         LRH-KRPV-PAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDS
                                                                                                                                                                                                                                                                                                                        DFSRDLMLAGTQQSVELKLALDQEQQKSKKLEESMRLLDEEMRRTDELLYQMIPKQVADR
                                                                                                                              NS---VYKVETIGDAYMVVAGAPDKDANHAERVCDMALDMVDAITDLKDPSTGQHLRIRV
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lla X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Llu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mckulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhonin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Schence 287:2185-2195(2000).
EMBL, AE003707, AAR55135.1;
RIJSBase, FBgn001858, CS DNA math
                                                                                       PROSITE: PS00095; C5_MTASE_2; UNKNOWN_1.
PROSITE: PS50125; GUANYLATE_CYCLASES_2;
SEQUENCE 690 AA; 78736 MW; 4B736D741
                                                                                       4B736D7413E168AA CRC64;
Length
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Score 929.5; DB Pred. No. 1.1e-6: 9; Mismatches 2: 5; DB 5; 1.1e-61; hes 231; Indels 49;

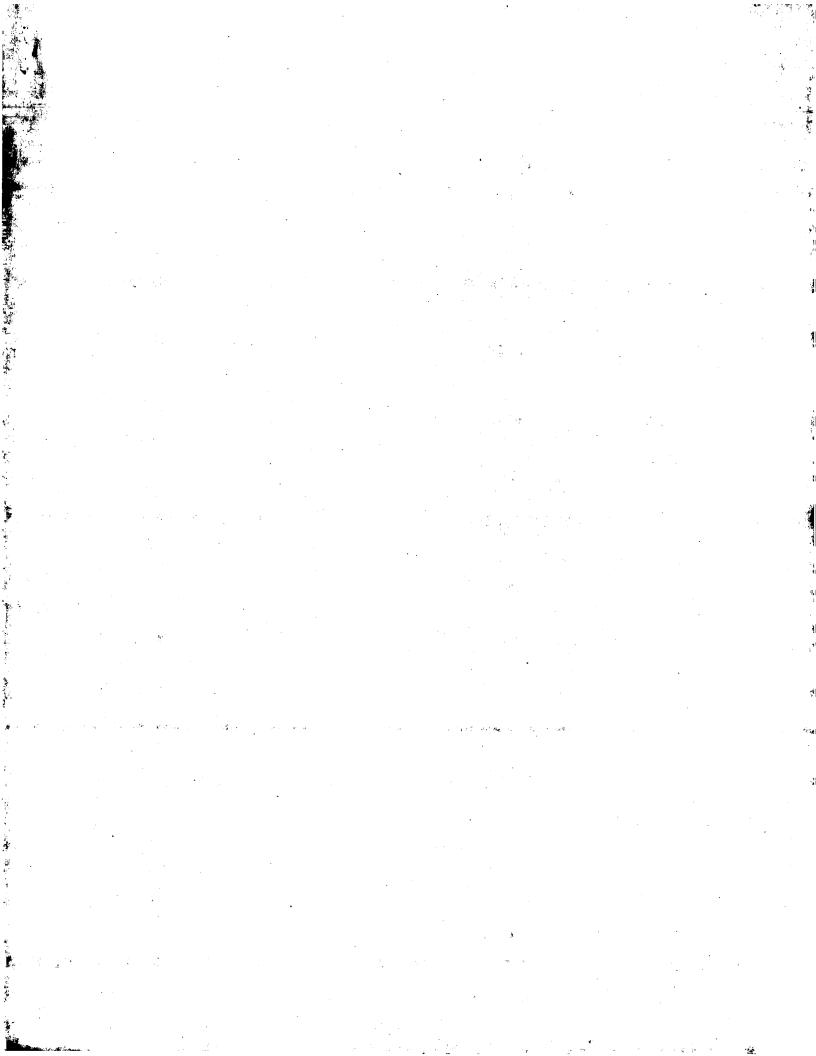
RCTDAEKGKGLILHYYSEREGLQDIVIGIIKTVAQQIHGTEIDMKVIQQR-------NEECDHTQFLIEEKESKEEDFYEDLDRFEENGTQESRISPYTFCKAFPFHIIFDRDLVVT MYGEVNHALELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLN MYGLLLENLSEY IKSVYGEEKWEDIRRQAGIDSP-SFSVHQVYPENLLQKLAKKAQQVLG VSERDFMDQMGVYFVGFVGQYGYDRVLSVLGRHMRDFLNGLDNLHEYLKFSYPRMRAPSF 120 60 230 59 178

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IVE	מעם	- AS	iva iva	Squence 2, Application United to 5237051 ENERAL INFORMATION: APPLICANT: Garbers, D. APPLICANT: Schulz, St. TITLE OF INVENTION: CORRESPONDENCE ADDRESS: ADDRESSEE: TILTON, I STREET: 100 South W. CITY: Chicago STATE: 111inois COUNTRY: U.S.A. ZIP: 60606-4002 COMPUTER READABLE FORM MEDIUM TYPE: PLOPPY COMPUTER: IBM PC CONPUTERING SYSTEM: PAPPLICATION DAVAPPLICATION DAVAPPLICATION DAVAPPLICATION UNMBER: FILING DATE: 199012 CURRENT APPLICATION UNMBER: FILING DATE: 199012 CURSIFICATION UNMBER: FILING TYPE: FILING PARTING SYSTEM: PROPERATION OF ASSISTMENT APPLICATION		
PEL	PEDI	1 6	Tive	Application US/07 Application US/07 2337051 Sigarbers, David Schulz, Stepha: SEQUENCES: 2 UDENCE ADDRESS: SEE: TILTON, FALL 100 South Wacke Chicago Illinois Illinois Illinois IVPE: Floppy dis TYPE: Jogopat TYPE: 19901206 B: Patentin Rele TYPE: 19901206 B: Patentin NUMBER: US/ DATE: 19901206 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CE/DOCKET NUMBER: 30 CHARACTERISTICS: NICATION INFORMAT TYPE: protein TYPE: protein	670 670 670 670 670 670 7722 7722 7722 7	
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GENERAL INFORMATION:
APPLICANT: Kaplan, Joshua M.
APPLICANT: Oppenhedmer, Allison J.
APPLICANT: Hart, Anne C.
ITILE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
ITILE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
FILE REFERENCE: 00786/353001
CURRENT APPLICATION NUMBER: US/08/864,785A
CURRENT APPLING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 1253
TYPE: PRT
ORGANISM: Caenorhabditis elegans
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                                                                              Sequence 2, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
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NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMVPEYRKFRPFTMNLMTNVSILFADIAGF----TKMSSNKSADELVNLLNDLFGRFDTL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTL 460
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                                                                AND USES THEREFOR
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Pred. No. 5.
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                                                                                                    ADENYLYL CYCLASE
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US-08-726-214-18
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US-08-726-214-2
                                                                                                                              Sequence 18, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Releg
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: Concurrent)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                          STREET: F. STREET: F. TOVAS
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      COUNTRY: United States ZIP: 77210
                                        STATE: Texas
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ZIP: 77210
                                                                                                  ADDRESSEE:
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                                                                              Arnold, White & Durkee
O. Box 4433
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US-08-726-214-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
            CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                            APPLICANT: Tang, Wei-Jen
APPLICANT: Gliman, Alfred G.
TITLE OF INVENTION: SOLUBLE:
TITLE OF INVENTION: AND USES
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                     COUNTRY:
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                                                                                                                                                     Texas
                                                                                                                                                                                   P.O. Box 4433
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MBER: US/08/726,214 Concurrently Herewith
                                                                                                                                                                                                                                            SOLUBLE MAMMALIAN AND USES THEREFOR
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                                                                                                                                     of America
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US-09-473-717-2
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Best Local S
Matches 136
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GENERAL INFORMATION:
APPLICANT: Storm, Daniel R.
APPLICANT: Hacker, Beth
APPLICANT: Tomlinson, James E
APPLICANT: COR Therapeutics,
APPLICANT: University of the APPLICANT: University of TITLE OF INVENTION: CLONING A
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                       Sequence 2, Application US/09473717 Patent No. 6372475
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LENGTH: 1248 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          1115 ASRMDSTGVSGRIQVPEETYLIL-----KDQGFAFDYRGEIYVKGISEQEGKIKTYFL 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1055 GHLCALADFSLALTESIQEINKHSFNNFELRIGISHGSVVAGVIGAKKPQYDIWGKTVNL 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 TSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLEHRGPVSMKGKKE---PMQVWFL 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 MRDEVFKSNLVCAFIVLLFITAIQSLLPSSRLMPMTI--QFSILIMLHSALVLITTAED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 L--DRFEENGT-------QESRISPYTFCKAFPFHIIFDRDLVVTQCGNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 LAQALHVQSGPE-----EINKRIEHTIDLRSGDKLRREHIKPFSLMFKDSSLEHKYSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSICHLALDMMEIAGQVQVDGE----SVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEMNNOGVECLELLNEIIADFDELLGEDRFQDIEKIKTIGSTYMAVSGLSPEKQQCEDKW 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVYKVETVGDKYMTVSGL-PE--PCIHHA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEMKDLREHNENMLRNILPGHVARHFLEKDRDNEELYSQSYDAVGVMFASIPGFADFYSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKCLPLILKTCCWINETYLARNVIIFASILINFLGAV--INILWCDFDKS--IPLKNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LEDEKKKTDTLLYSVLPPSVANEL----RHKRPVPAKRYDNVTILFSGIVGFNAFCSK 436
                            Tomlinson, James E. .
COR Therapeutics, Inc.
University of Washington
VENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1248 amino acids
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Pred. No. 2.2e-21;
""smatches 209;
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44481-5029-01-US

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PRIOR APPLICATION NUMBER: PCT/US98/135/
PRIOR FILING DATE: 1998-07-01
PRIOR PPLICATION NUMBER: 60/098,559
PRIOR FILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 08/886,440
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
UNMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1305
TYPE: PRT
ORGANISM: Mus musculus
US-08-864-785-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Kaplan, Joshua M.
APPLICANT: Oppenheimer, Allison J.
APPLICANT: Hart, Anne C.
APPLICANT: Hart, Anne C.
TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
                                                                                                                                                                                                                                              Query Match 9.0%;
Best Local Similarity 31.2%;
Matches 74; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08864785A Patent No. 6329566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 00786/353001
CURRENT APPLICATION NUMBER: US/08/864,785A
CURRENT FILING DATE: 1997-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/473,717
CURRENT FILING DATE: 1999-12-29
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Local Similarity 31.2%;
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                                                                                                       RPVPAKRYDNYTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFV 469
                                                                                                                                                              LEVEKALKERMIHSVMPRIIADDLMKQGDEESENSVKRHATSSPKNRKKKSSIQKAPIAF 382
                                                                                                                                                                                                       LEDEKKKTDTLLYSVLPPSVANEL-----RHK-----RHK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPVPAKRYDNYTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFV 469
  EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV
                                                                             RPFKMQQIEEVSILFADIVGF----TKMSANKSAHALVGLLNDLFGRFDRLCEQTK---C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 291.5; DB 4;
Pred. No. 1.2e-19;
Prematches 72;
                                                                                                                                                                                                                                              Score 291.5; DB 4;
Pred. No. 1.2e-19;
4; Mismatches 72;
                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                       Length 1305;
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495
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                                                                                                                 ; OTHER INFORMATION: HYPOTHETICAL: US-09-398-193-2
                                                                                                                                                            SEQ ID NO 2
LENGTH: 1353
TYPE: PRT
ORGANISM: Mouse
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; OTHER INFORMATION: HYPOTHETICAL :
US-08-894-173-2
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US-08-894-173-2
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LENGTH: 1353
TYPE: PRT
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APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cycla
FILE REFERENCE: P24360-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase
FILE REFERENCE: P14716C
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09398193 Patent No. 6197581
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Patent No. 609061
                                                  Matches
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Best Local
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/894,173A CURRENT FILING DATE: 1997-08-13 NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                                                                SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mouse
                                                                                                                                                FEATURE:
383 LEDEKKKTDTLLYSVLPPSVANEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 LCGILGMRRFKFDVWSNDVNLANLMEQLGVAGKVHISEATAKYL-----DDRYEME 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 VTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLE 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCGILGMRRFKFDVWSNDVNLANLMEQLGVAGKVHISEATAKYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLE 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPFKMQQIEEVSILFADIVGF----TKMSANKSAHALVGLLNDLFGRFDRLCEQTK---C 435
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                                                             9.0%;
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Pred. No. 1.3e
44; Mismatches
                                                              Score 291.5;
Pred. No. 1.
                                                  Mismatches
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RESULT 11
US-08-726-214-10
19-08-726-214-10
; Sequence 10, Application US/08726214
; Patent No. 6107076
; Patent No. 6107076
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US-09-473-717-3
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LENGTH: 1353
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/473,717
CURRENT ELLING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1997-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF TITLE OF INVENTION: CYCLASE
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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FILING DATE: 1997-07-01
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Similarity 31.2%; Pred. No. 1.
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Best Local Similarity
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APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT IMPORMATION:
NAME: Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: AN NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                            RKEEKAMIAKMNRQRTNS
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milarity 23.58;
Conservative 84
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Pred. No. 2e-19;
34; Mismatches 1
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US-08-726-214-6
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Patent No. 6107/076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.9%;
Best Local Similarity 21.8%;
Matches 119; Conservative 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
TITLE OF INVENTION: AND USES THEREFOR
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LENGTH: 1144 amino aci
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
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ZIP: 77210
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MKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIH---
                                                                                                                                                  LYLSD--IPLHDATRDL-VLLGEQFREEYKLTQELEILTDRLQLTLRALEDEKKK-----
                                                                                                                                                                                       --VSHMVKLTLMLLVTGA-VTAINLYAWCPVFDEYDHKRFQEKDSPMVALEKMQVLSTPG
                                                                                                                                                                                                                            EGLLDVEKLECEDELTGTEISCLRLKGQMIYLPEADSILFLCSPSVM----NLDDLTRRG
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                                       RWNEALVTNMLPEHVARHFLGSKKRDEELYSQSYDEIGVMFASLPNFADFYTEESINNGG
                                                                          --TDTLLYSVLPPSVANEL----RHKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGA
                                                                                                             LNGTDSRLPLVPSKYSMTVMMFVMMLSFYYFSRHVEKLARTLFLWKIEVHDQKERVYEMR
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Pred. No. 3.1e-19;
14; Mismatches 201;
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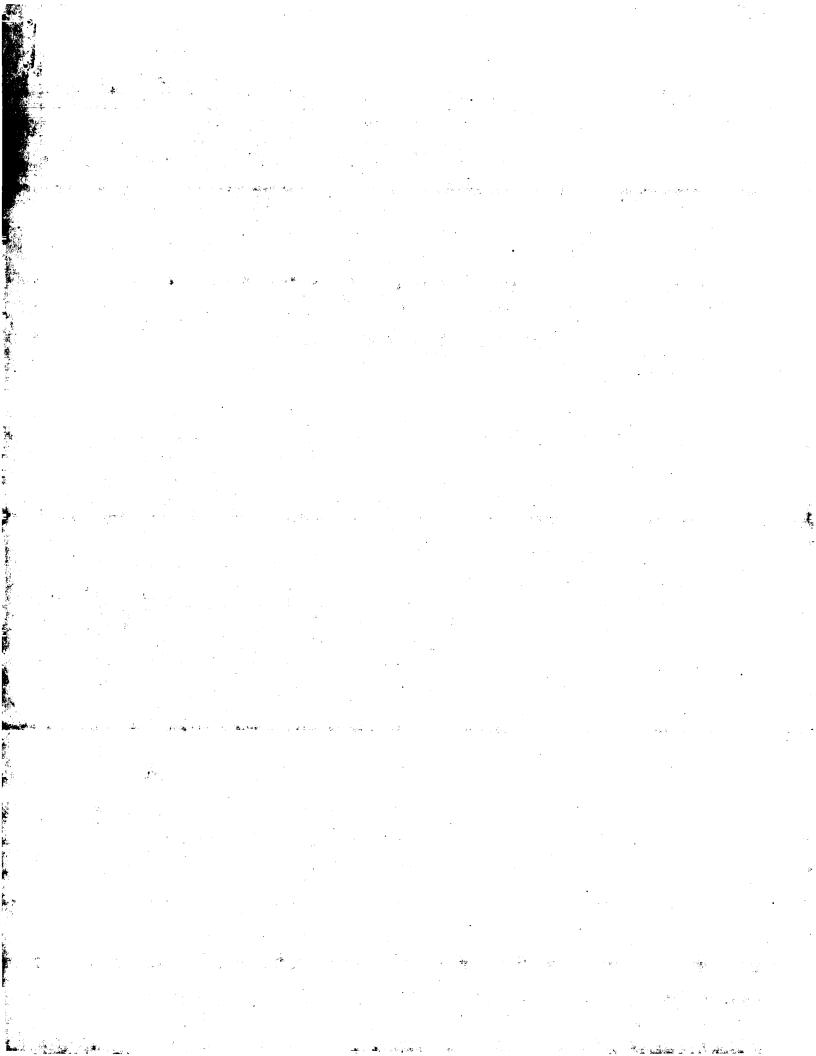
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RESULT 14
US-08-726-214-14
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US-09-398-193-99
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Patent No. 6107076
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/398,193
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 104
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin
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TYPE: PRT
                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
COMPUTER READABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                               COUNTRY:
                                                         STATE:
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                                                       Houston: Texas
                   77210
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 FORM
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30.8%; Pred. No. 8.2e-19;
                                       of America
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US-09-474-076-2
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                                                   PRIOR APPLICATION NUMBER:
PRIOR EILING DATE: 1997-07
PRIOR APPLICATION NUMBER:
PRIOR EILING DATE: 1997-07
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                       FILE REFERENCE: 44481-5028-01-US
CURRENT APPLICATION NUMBER: US/09/474,076
CURRENT FILING DATE: 1999-12-12
                                                                                                                                                                                                                                              APPLICANT: Tomlinson, James E.
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
TITLE OF INVENTION: CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                      SOFTWARE:
LENGTH: 1168
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REFERENCE/DOCKET NUMBER: UT.
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                ID NO 2
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    PatentIn Ver.
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Pred. No. 7.2e-19;
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; ORGANISM: human type VI adenylyl cyclase
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Best Local
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                                 574 SPENSDP-----QFHLEH---RGPVSMKGKKEPMQVWFLSRKNTGTEE 613
                                                                     466
                                                                                                 514 GESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLM 573
                                                                                                                                     409 ARFDKLAAEN---HCLRIKILGDCYYCVSGLPEARADHAHCCVEMGVDMIEAISLVREVT 465
                                                                                                                                                                     455 TREDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQV-QVD 513
                                                                                                                                                                                                          355
                                                                                                                                                                                                                                          407
                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                          347 DATRDIVLIGEQFREEYKLTQELEILTDRIQLTLRALEDEKKKTDTLLYSVLPPSVANEL 406
                                                                                                                                                                                                                                                                                                                                              262 LSGLGLSTLHLILAWQLNRGDAFLWKQLGANVLLFLCT---
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                        R------HKRPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLY
                                                                                                                                                                                                                                                                          ----NVIGICTHYPAEVSQRQAFQETRGYIQARLH-LQHENRQQERLLLSVLPQHVAMEM
GDYEVEPGRGGERNAYLKEQHIETFLILG-ASQKRKEEKAMLAKLQRTRANSME
                                                                 GVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHMEAGGRAGRIHITRATLQYLN
                                                                                                                                                                                                       KEDINTKKEDMMFHK--IYIQKHDNVSILFADIEGFTSLASQCT----AQELVMTLNELF 408
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 282.5; DB; Pred. No. 8e-19; 61; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                73;
 578
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                        454
                                                                                                                                                                                                                                                                                                                                                                              346
                                                                                                                                                                                                                                                                          354
                                                                                                                                                                                                                                                                                                                                            299
```

Search completed: June 27, 2003, 13:05:59
Job time: 14.7678 secs



GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 13:05:32; Search time 32.6287 Seconds
(without alignments)
2080.112 Million cell updates/sec

Title: Perfect score: US-09-762-767A-4
3231
1 MYGFVNHALELLVIRNYGPE.....QVWFLSRKNTGTEETKQDDD 619

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters:

424699

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database 4: 5: 6: 7: 7: 9: 9: 110: 112: 113: Published_Applications_AA: * /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	₽B	ID	Description
1	789.5	24.4	690	إو	US-10-205-823-162	Sequence 162, App
2	778	24.1	691	9	US-09-952-213D-2	Sequence 2, Appli
ω		12.6	1073	10	US-09-819-249-2	•
4	405.5	12.6	1073	o	US-10-157-031-18	•
u	291.5	9.0	1294	12	US-10-071-223-2	N
6	291.5	9.0	1353	10	US-09-751-100B-2	•
7	291.5	9.0	1353	12	US-10-071-223-3	•
8	289	8.9	1080	9	US-10-282-942-2	>
9	283.5	8.8	1353	10	US-09-751-100B-99	Sequence 99, Appl
10	282.5	8.7	1168	9	US-10-201-000-2	Sequence 2, Appli
11	282.5	8.7	1168	10	US-09-750-240-11	Sequence 11, Appl
12	278.5	8.6	604	10	US-09-750-240-4	Sequence 4, Appli
13	278.5	8.6	1167	10	US-09-750-240-6	-
14	278	8.6	1261	9	US-10-175-158-2	Sequence 2, Appli
15	269.5	8.3	257	9	US-09-989-442-95	Sequence 95, Appl
16	269.5	8.3	302	10	US-09-915-582-50	\sim
17	269.5	8.3	1077	9	US-10-121-911-1	
18	265.5	8.2	1167	10	US-09-750-240-13	Sequence 13, Appl
19	264	8.2	241	9	US-09-764-868-794	Sequence 794, App

Query Match Best Local Similarity

24.4%;

Score 789.5; DB 9; Pred. No. 5.3e-60;

Length 690;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
131	131	131	131	131	131	131.5	134.5	137	137	137	137.5	149	149	172.5	172.5	173	173	175.5	175.5	175.5	175.5	234.5	242	259.5	264
4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.3	4.6	4.6	5. 3	5. 3	5.4	5.4	5.4	5.4	5.4	5.4	7.3	7.5	8.0	8.2
85	85	85	85	85	24	90	90	85	85	85	88	107	107	112	112	419	419	722	722	670	670	311	225	855	241
10	10	10	10	10	9	10	10	10	10	10	10	10	10	10	10	ဖ	9	9	9	9	9	10	φ	10	9
US-09-751-100B-58	US-09-751-100B-57	US-09-751-100B-56	US-09-751-100B-55	US-09-751-100B-54	US-10-106-698-5238	US-09-751-100B-48	0 US-09-751-100B-49	US-09-751-100B-61	US-09-751-100B-60	US-09-751-100B-59	US-09-751-100B-62	US-09-844-353A-76	US-09-205-658-76	US-09-844-353A-75	US-09-205-658-75	US-09-880-505-125	US-10-051-643-125	US-09-880-505-174	US-10-051-643-174	US-09-880-505-178	US-10-051-643-178	US-09-925-297-515	US-09-989-442-92	US-09-925-297-811	US-09-989-442-141
58,	57,	56,		Sequence 54, Appl	5238,	48,		61,	60,	59,	-	76,	76,	75,	75,	Sequence 125, App	Sequence 125, App	Sequence 174, App	174,	•	Sequence 178, App		Sequence 92, Appl	Sequence 811, App	Sequence 141, App

ALIGNMENTS

; PRIOR FILING DATE: 2002-03-05 ; NUMBER OF SEQ ID NOS: 455 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 162 ; LENGTH: 690 ; TYPE: PRT ; ORCANISM: Homo sapiens US-10-205-823-162	APPLICANT: Endege, Wilson O. APPLICANT: Gannavarapu, Manjula APPLICANT: Gannavarapu, Manjula APPLICANT: Gorbatcheva, Bella APPLICANT: Gorbatcheva, Bella APPLICANT: Kamatkar, Shubhangi APPLICANT: Wonsey, Angela M. APPLICANT: Glatt, Karen APPLICANT: Glatt, Karen APPLICANT: Glatt, Karen APPLICANT: Anderson, Dustin TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: THERAPY OF PROSTATE CANCER	3-162 62, Applican No. US200 FORMATION: Schlegel
	PREVENTION,	
	AND	

Matches

207;

101

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RESULT 2
US-09-952-213D-2
; Sequence 2, Application US/09952213D
; Publication No. US20030096240A1
                                                                                                                                                                                                                                                                                                                                               APPLICANT: KRUMENACKER, J. S.
APPLICANT: MARTIN, E.
TITLE OF INVENTION: GENOMIC ORGANIZATION OF PILE REFERENCE: UTSH: 252US
CURRENT APPLICATION NUMBER: US/09/952,213D
CURRENT FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 VVGGTLKDFLNSFSTLLKQSSHCQEAGKRGRLEDASILCLDKE-DDFLHVYYFFPKRTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDELTGTEISCLRLKGQM 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVIGIIKTVAQQIHGTEIDMKVIQQRNEECDHTQ-----FLIEEKESKEEDFY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIKESRKSLEREDFEKTIAEQAVAAGVPV-----EVIKESLGEEVFKICYEED-ENILG 153
                                           LNLALQRTLAKHKIEENRKSSEKED----LEKIIAEEA----IAAGAPVEALK-----D
                                                                     LELLVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEILQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSRTETTGEKGKINVSEYTYRCL-------MSPENSDPQFHLEHRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAVQIALMALKMMELSDEVMSPHGEPIKMRIGLHSGSVFAGVVGVKMPRYCLFGNNVTL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAICSQCS----PLQVITMLNALYTRFDQQCGELD---VYKVETIGDAYCVAGGLHKESD 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAFCSKHASGEGAMKIVNLLNDLYTREDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCI 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYLPEADSILFLCSPSYMNLDDLTRRGLYLSDIPLHDATRDLYLLGEQFREEYKLTQELE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LILPGIIKAAAHVLYETEVEVSLM----PPCFHNDCSEFVNQPYLLYSVHMKSTKPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLDEEGQFLVRIIYDDSKTYDLVAAASKVLNLNAGEIL-QMFGKMFFVFCQESGYDTILR 88
  MFGKMFFVFCQESGYDTILRVLGSNVREFLQNLDAL-----HDHLATIYPGMRAPSFRCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HHARSICHLALDMEIAGQV-QVDGESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLKATLEQAHQALEEEKKKTVDLLCSIFPCEVAQQLWQGQVVQAKKFSNVTMLFSDIVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILTDRLQLTLRALEDEKKKTDTLLYSVLPPSVANELRHKRPVPAKRYDNVTILFSGIVGF 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEYFEILTPKINQTFSGIMTMLNMQFVVRVRRWDNSVKK------SSRVMDLKGQM 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLGSNVREFLQNLDAL-----HDHLATIYPGMRAPSFRCTDAEKGKGLILHYYSEREGLQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELPPNFPSEIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYIVESSAILFLGSPCVDRLEDFTGRGLYLSDIPIHNALRDVVLIGEQARAQDGLKKRLG
                                                                                                                                     Conservative
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                                                                                                                                     105;
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                                                                                                                                Score 778; DB 9;
Pred. No. 5.3e-59;
DS; Mismatches 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE AND
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                                                                                                                                                                            Length 691;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                Gaps
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                                              134
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                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/819,249
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/192,229
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 1073
TYPE: PRT
CORGANISM: Homo sapiens
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US-09-819-249-2
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                                                                                                                                                          Matches
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09819249
Patent No. US20010029019A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Waldman, Scott A.
APPLICANT: Park, Jason
APPLICANT: Schulz, Stephanie
TITLE OF INVENTION: Compositions And Methods
TITLE OF INVENTION: Alimentary Canal Origin
FILE REFERENCE: TJUZ412
                                                                245 VIIMCGGPEFLYKLKGDRAVAEDIVIILVDLFNDQYLEDNVTAPDYMKNVLVLTLSPGNS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 PVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFVY
                    67 L----
                                                                                                     12 LVIRNYGPEVWEDIKKEAQLDEEGQFLVRIIYDDSKTYDLVAAAS-----KVLNLNAGEI 66
                                                                                                                                                          180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGVVGVKMPRYCLFGNNVTLANKFESCSVPRKINVSPTTYRLLKDCPGFVFTPRSREELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCL------MSPENSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVETIGDAYCVAGGLHRESDTHAVQIALMALKMMELSNEVMSPHGEPIKMRIGLHSGSVF
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                                                                                                                                                       Conservative
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                                                                                                                                                                          12.6%;
22.6%;
                                                                                                                                                   117;
                                                                                                                                                   Score 407.5; DB 10;
Pred. No. 2e-26;
7; Mismatches 274;
-OMFGKMFFVFCQE--
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                  ---SGYD
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; ORGANISM: Mus musculus US-09-952-213D-2

Query Match Best Local :

l Similarity 213; Conserv

; NUMBER OF SEQ ID NOS: 15 SOFTWARE: PatentIn Ver. 2 SEQ ID NO 2 LENGTH: 691 TYPE: PRT

APPLICANT: MURAD, FEI APPLICANT: SHARINA,

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US-10-157-031-18
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; ORGANISM: Homo sapiens
US-10-157-031-18
                                             NUMBER OF SEQ ID NOS: 415
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 1073
                                                                                                                                                                                                                                                                                  Sequence 18, Application US/10157031 Publication No. US20030108890A1
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                               APPLICANT: Baranova, A. V.
APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed FILE REFERENCE: 2760-103
                                                                                                               CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
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US-10-071-223-2
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Matches 103
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Matches
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APPLICANT: Storm, Daniel
APPLICANT: Hacker, Beth
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                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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PRIOR APPLICATION NUMBER: 09/473,717
PRIOR PILLING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR APPLICATION NUMBER: PCT/US98/13541
PRIOR FILLING DATE: 1998-07-01
PRIOR FILLING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR FILLING DATE: 1997-07-01
PRIOR FILLING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: human type IX adenylyl cyclase US-10-071-223-2
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APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5029-02-US
CURRENT APPLICATION NUMBER: US/10/071,223
CURRENT FILING DATE: 2002-02-11
                                                                                                                                                                                                                                                                              323 LEVEKALKERMIHSVMPRIIADDIMKQGDEESENSVKRHATSSPKNRKKKSSIQKAPIAF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 LLGEQFREEYKLTQELEILTDRLQLTLRALED------EKKKTDTLLYSVLPPSV
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                                                                                                                                                               RPFKMQQIEEVSILFADIVGF----TKMSANKSAHALVGLLNDLFGRFDRLCEETK---C 435
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                                                                                           YKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQ-VQVDGESVQITIGIHTGEV 528
                                                                                                                                                                                                                         RPVPAKRYDNVTILFSGIVGFNAFCSKHASGEGAMKIVNLLNDLYTRFDTLTDSRKNPFV 469
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VTGVIGORMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMSPENSDPQFHLE
                                                       EKISTLGDCYYCVAGCPEPRADHAYCCIEMGLGMIKAIEQFCQEKKEMVNMRVGVHTGTV
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                                                                                                                                                                                                                                                                                                                                                                                           Score 291.5; DB 12.
Pred. No. 3.5e-16;
4; Mismatches 72;
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RESULT 7
US-10-071-223-3
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US-09-751-100B-2
US-10-071-223-3
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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                                                                                                                                                                  SEQ ID NO 3
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PRIOR APPLICATION NUMBER: PCT/US98/1
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/098,559
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 44481-5029-02-US
CURRENT APPLICATION NUMBER: US/10/071,223
CURRENT FILING DATE: 2002-02-11
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                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/886,440
PRIOR FILING DATE: 1997-07-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: COR Therapeutics, Inc.
APPLICANT: University of Washington
TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
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TYPE: PRT
                              ORGANISM: murine
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Pred. No. 3.7e-16;
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-282-942-2
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US-10-282-942-2
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PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Best Local S
Matches 74
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APPLICANT: S1105 Santiago, Inmaculada
APPLICANT: S1105 SENTIAGO, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS
FILE REFERENCE: MPIO1-240PLN
CURRENT APPLICATION UNMBER: US/10/282,942
CURRENT FILING DATE: 2002-10-29
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                                                                                                                                                                                                                                                                                                                                                      168 --GFTTPSVRVGLQLL----ANAVIFLCG----NLTGAFHKH-----QMQDASRDL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 IYRVLPQLQPGNCSLLSVFSLVRPHIDISFHGILSHINTVFVLRSKEGLLDVEKLECEDE 295
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Similarity 26.3%;
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                                      SVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCL 572
                                                                                      FDQIAKANE---CMRIKILGDCYYCVSGLPVSLPTHARNCVKMGLDMCQAIKQVREATGV 367
DINMRVGIHSGNVLCGVIGLRKWQYDVWSHDVSLANRMEAAGVPGRVHITEATLKHL
                                                                                                                                FDTLTDSRKNPFVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQV-QVDGE 515
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31.2%; Pred. No. 3.7e-16;
44. Mismatches 72;
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Pred. No. 4.4e-16;
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US-10-201-000-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10201000 Publication No. US20020187540A1 GENERAL INFORMATION:
                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 99
LENGTH: 1353
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Best Local (
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CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/201,000 CURRENT FILING DATE: 2002-07-24 PRIOR APPLICATION NUMBER: US/09/474,076 PRIOR FILING DATE: 1999-12-12 PRIOR APPLICATION NUMBER: PCT/US98/13694 PRIOR FILING DATE: 1998-07-01
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 08/886,550
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 44481-5028-01-US
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262 LSGLGLSTLHLILAWQLNRGDAFLWKQLGANVLLFLCT
                               296 LTGTEISCLRL------KGQMIYLPE--ADSILFLCSPSVMNLDDLTRRGLYLSDIPLH 346
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26.6%;
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Pred. No. 1.9e-15;
Pred. No. 1.9e-15;
                                                                   Score 282.5; DB 9;
Pred. No. 1.8e-15;
1; Mismatches 126;
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US-09-750-240-11
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-5
PRIOR FILING DATE: 1997-09-05
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Best Local ;
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LENGTH: 1168
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Patent No. US200
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 08/708,661
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                    455 TREDILIDSRKNPEVYKVETVGDKYMTVSGLPEPCIHHARSICHLALDMMEIAGQV-QVD
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                                                            KEDINTKKEDMMFHK--IYIQKHDNVSILFADIEGFTSLASQCT----AQELVMTLNELF
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Pred. No. 1.8e-
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US-09-750-240-4
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PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-75
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.6%;
Best Local Similarity 27.1%;
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TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/708,661
PRIOR FILING DATE: 1996-09-05
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                              315 DYEVEP 320
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                                                                                                                                   ESVQITIGIHTGEVVTGVIGQRMPRYCLFGNTVNLTSRTETTGEKGKINVSEYTYRCLMS
                                                                                                                                                                       RFDKLAAEN---HCLRIKILGDCYYCVSGLPEARADHAHCCVEMGVDMIEAISLVREVTG
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Sequence 2, Application US/10175158

Publication No. US20030008371A1

GEMERAL INFORMATION:
APPLICANT: Tomlinson, James
APPLICANT: Cor Therapeutics, Inc.
APPLICANT: Cor Therapeutics AD CHARACTERIZATION
TITLE OF INVENTION: CLONING AND CHARACTERIZATION
TITLE OF INVENTION: CYCLASE
FILE REFERENCE: 4481-5027-01-US
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TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
TITLE OF INVENTION: FAILURE
FILE REFERENCE: 220002056723
CURRENT APPLICATION NUMBER: US/09/750,240
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/472,667
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-01-16
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 09/008,097
PRIOR APPLICATION NUMBER: US 08/924,757
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: US 60/048,933
PRIOR FILING DATE: 1997-09-05
RESULT 14
US-10-175-158-2
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Best Local Similarity
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APPLICANT:
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Pred. No. 4e-15;
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NUMBER: US/10/175,158

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; TYPE: PRT
; ORGANISM: human type V adenylyl cyclase
US-10-175-158-2
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US-09-989-442-95
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PRIOR APPLICATION NUMBER: US/09/473,716
PRIOR FILING DATE: 1999-12-29
PRIOR PPLICATION NUMBER: PCT/US98/13540
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR APPLICATION NUMBER: 60/070,901
PRIOR FILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 09/886,362
PRIOR FILING DATE: 1997-07-01
NUMBER: OF SEQ ID NOS: 2
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Publication No. US20030013649A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            ILE REFERENCE: PJZ08
                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                FILING DATE: 2000-UB-14
APPLICATION NUMBER: 60/220,963
BTILING DATE: 2000-07-26
                                                             APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
                                                                                                                                                                                                        APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28 APPLICATION NUMBER: 60/217,487
                                                                                                                                                                                                                                                         FILING DATE: 2000-01-31
APPLICATION NUMBER: 60/180,628
FILING DATE: 2000-02-04
                                                                                                                                                                            APPLICATION NUMBER: 60/225,758
APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14 APPLICATION NUMBER: 60/225,757 FILING DATE: 2000-08-14
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                                                                                                                                                                                                                                                                                                                                           60/231,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/232,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60/232,399
                                                                                                                                                                                                                                                                                                                                                                   60/246,475
                                                                                                                                                                                                                                                                                                                                                                                           60/241,221
                                                                                                                                                                                                                                                                                                                                                                                                                     60/241,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/232,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60/233,063
                                                                                                                                                                                                                                                                                                                   60/233,065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60/233,064
                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                   Score 269.5; DB 9;
Pred. No. 2.4e-15;
8; Mismatches 100;
251
                      605
                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                      Indels
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257; 25;

Gaps

ø

417

60

177

Search completed: June 27, Job time : 34.6287 secs 2003, 13:17:13